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Minimum
Maximum
                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                         Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                              DB seq
                                                                                                                                                                                                                                                                                                                                                                                                                                              length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                   GenEmbl:*
1: gb_ba:*
2: gb_htg:
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3661
1 ggagcggggcgcc
  2054640 segs, 14551402878 residues
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Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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gb_htg:*
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gb_pat:*
gb_ph:*
                           em_htg_mus:*
em_htg_pln:*
em_htg_rod:*
em_htg_mam:*
em_htg_vrt:*
em_htg_vrt:*
em_htgo_hum:*
em_htgo_mus:*
em_htgo_other:*
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em_vi:*
em_htg_hum:*
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gb_sts:*
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17096.497 Million cell updates/sec
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

C C 4 4 4 4 4 4 8 8 8 9 0 1 1 3 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	c 27 32 22 23 32 23 33 33 33 33 33 33 33 33	16 17 19 20 21 22 23 25	2 2 2 3 3 4 4 4 5 5 6 6 7 7 7 11 1 1 1 1 1 1 1 1 1 1 1 1 1	Result No.
460.8 460.8 458.4 458.4 453 435.6 432.8	51 507 507 50 76 74 71 46 46	749.4 585 584.8 576.6 575.8 551. 551. 541.8 541.8	3542.6 3032.8 3097.4 2626.2 2595.2 2595.2 2511.6 1724.4 1632.8 919.6 919.6 749.4	Score
112.66 112.66 112.66 111.99	2222333344			% Query Match
3617 3617 5347 3718 3561 1086 3050 3777	3630 4194 3886 4315 1900 1900 1900 1903 192364 192364 199345 157466	300412 2529 2726 3480 3779 3114 3126 3132 3549 3549 3590 3607	5227 5227 3810 3111 3384 3505 3148 3505 3148 2568 3288 3445 3445 3445 3445 3445 3445 3445 34	Length
10 3 5 6	10 22 20 10	3 5 5 5 5 5 5 7 7 7 7 7 7 7 7 7 7 7 7 7	10 10 10 10 10 10 10 10 10 2 3	DB
AX394541 HSA310570 AK092877 GGBBMIBA AF051353 DRONEWMYO HSM803609 MMMYOSINI	MMMIHCL MUSMYOSIX DMU07595 AY075567 AF380932 AF380933 RRMYR4 AC084102 BC028071 AL591440	ABO03471 RNU25148 AF009960 GDU04049 BOVMYHC GGBBMI AVBMI AVBMI AF027026 AF107026 AF105424 RNMYR1A	A 2007255 BC021481 RNMYR2 MMU96723 HSMYOIB BTW03420 BTWYOIBA MMMIB BCU14382 RCU14382 RCU14382 AC012834 AC012834 AC012834 AC012834 AC012007	ID
AX394541 Sequence AX310570 Homo sapi AK092877 Homo sapi X70400 G.gallus mR X70400 G.gallus mR AF051353 Acanthamo L13070 Drosophila AL832302 Homo sapi X97650 M.musculus	0 2 333		AY007255 Mus muscu BC021481 Mus muscu X74800 R.norvegicu U96723 Mus musculu X98507 H.sapiens m U03420 Bos taurus Z22852 B.taurus my X99638 M.musculus U14382 Rana catesb U14349 Rana catesb U14549 Rana catesb AY069044 Drosophila AC012834 Drosophil AC010807 Drosophil AC01087 Drosophil	Description

## ALIGNMENTS

AUTHORS	REFERENCE	ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	Locus	AY007255	RESULT 1
Pestic-Dragovich,L., Stojiljkovic,L., Philimonenko,A.A., Nowak,G., Ke,Y., Settlage,R.E., Shabanowitz,J., Hunt,D.F., Hozak,P. and de Lanerolle,P.	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 3663)	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Mus musculus.		AY007255.1 GI:11067001	AY007255	Mus musculus nuclear myosin I beta mRNA, complete cds.	AY007255 3663 bp mRNA linear ROD 01-NOV-2000		

Pred. No.

is the number of results predicted by chance to have a

FEATURES

Source

JOURNAL

Stoj

iljkovic, L.

TITLE JOURNAL REFERENCE AUTHORS TITLE

A Myosin I Isoform in the Nucleus Science (2000) In press

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421 GAGACTGCTCCAGTTCTATGCAGAGACCTGCCCAGCCCCTGAACGGGGTGGCGCAGTGCG 480
                                                                                                  301 AGTACCACCTCATTTGTTTGCAGTGGCTGACACTGTATACCGGGCACTTCGTACTGAGCG 360
                                                                                                                                                                        301 AGTACCACCTCATTTGCTTTGCAGTGGCTGACACTGTATACCGGGCACTTCGTACTGAGCG 360
                                                                                                                                                                                                                241 NGACCTACAGATCTACAGCCGGCAGCATATGGAAGGCTACCGTGGTGTCTCAGTTTCTATGA 300
                                                                                                                                                                                                                                241 AGACCTACAGATCTACAGCCGGCAGCATATGGAACGCTACCGTGGTGTCAGTTTCTATGA 300
                                                                                                                                                                                                                                                                      1 GGAGCGGGGCGCCGGGTCCGGCAGGATGCGCTACCGGGCATCGGCCCTGGGCAGTGACGG 60
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                                                                                                                                                                                                                                                                                                                                                                                   GGTTCGAGTGACCATGGAGAGCGCCTTGACTGCCCGAGACCGGGTAGGGGTGCCAGGACTT 120
                                                                                                                                                                                                                                                                                                                                                                                                 GGTTCGACTGACCATGGAGAGCGCCTTGACTGCCCGAGACCGGGTAGGGGTGCAGGACTT 120
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60; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (18-AUG-2000) Physiology and Biophysics, University Illinois at Chicago, 835 S. Wolcott, Chicago, IL 60612, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IENLERGERULI YN IGPULOSHOW ROLLT SAGURY DE SALTARDRY GVODFYLLENFTSEAAF TVERALRTERERULI YN IGPULOSHOW ROLLT SROHMEN FROUGHT SEAAF VLEARENARTERROAM ISGESGAGKTEAT KRLLOY AETCRAEBERGARDALLENGE SAGURTEAR ROLLOY AETCRAEBERGARDRLLOSH PUEARENARTLRANDNS SREGKYMD VOEDFKOAD VOEDFYL SYLLEK SKYVHOLHGERRE FROM THE STANDARD SKERFKY MD VOEDFKOAD VOEDFYL SYLLEK SKYVHOLHGERRE ROTT VLGLID IY GEFURDA SKERFKY MD VOEDFYKOAD VOEDFYL SYLLEK SKYVHOLHGERRE ROTT VLGLID IY GEFURDHAAD AARDALAKAN YS RTETWLYKI TRLLOY EETT LEAL DAD YR RKSID KE BERKE KOI ISILDERGLE ROEDFYL VRKI INRSLASKDAES SWEDN SKELSDKKE PETVATOR KASILLOLVE ILRSKE PAY IR CILL KE MOES SANDAES SWEDN SKELSDKKE PETVATOR KASILLOLVE ILRSKE PAY IR CILL KE MOES SANDAKOR STALLOS WORTH STANDAKOR SAICIOS WORTH FIRE FRILLATEDS LEVROSLAFY IN FORDOG VAN LYRH IR GYK PET Y KROTT SKET FORDE SKENDEN SKET FOR FYRIFT FREATED SKENDE SKENDEN FORDOG VAN LYRH IN SKET FKOR SKOTT SKET SKENDAKOR SAICIOS WORTH SKENDE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.7%; Score 3649; DI
100.0%; Pred. No. 0;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/product="nuclear myosin I beta"
/protein_id="AAG02570.1"
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/db_xref="taxon:10090"
/chromosome="11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 10; Length 3663;
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1501 GAAGTTGGAGGACACTGTGAAGCCCCACCCTCACTTCCTGACGCACAAGCTCGCTGACCA 1560
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                                         1441 CTCCATCTTGGATGAAGAGTGCCTGCGTCCTGGGGGAGGCCACGGACCTGACCTTTCTGGA 1500
                                                         1441 CTCCATCTTGGATGAAGAGTGCCTGGGTCCTGGGGAGGCCACGGACCTGACCTTTCTGGA 1500
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                                                                                                    1381 CCAGTACTTCAACAACAAGATCATCTGTGACCTGGTAGAGGAGAAGTTCAAGGGCATCAT
                                                                                                               1381 CCAGTACTTCAACAACAACAACCATCATCTGTGACCTCGTAGAGGAGAAGTTCAAGGGCATCAT 1440
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                                                                                                                                                    1321 GCTGACTCTCAAGTCGGAGCAGGAAGAATACGAGGCTGAGGGCATCGCGTGGGAACCTGT 1380
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     841 GTCCGTCATTGACTTCACTGAGGATGAAGTGGAGGACTTGCTCAGCATCGTGGCCAGCGT 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         721 TCTCCGTCGGCTGGGCTTGGAACGGAACCCCCAGAGCTACTTGTACCTGGTGAAGGGCCA 780
721 TCTCCGTCGGCTGGGCTTGGAACGGAACCGCAGAGCTACTTGTACCTGGTGAAGGGCCA 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       661 TCACGGAGAGCGGAACTTCCACGTCTTTTACCAGCTACTGGAGGGGGGCGACGAGGAGAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 601 CCCCGTGGGAGGCCACATTCTCAGTTACCTCCTGGAAAAGTCCCGGGTGGTGCACCAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   541 CAACGATAACTCCAGCCGGTTTGGAAAGTACATGGATGTGCAGTTTGACTTCAAGGGTGC 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   541 CAACGATAACTCCAGCCGGTTTGGAAAGTACATGGATGTGCAGTTTGACTTCAAGGGTGC 600
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Ouery Match Best Local Sim! Matches 3660;

61 61 DASE COUNT

865 a

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В	1501	GAAGTTGGAGGACACTGTCAAGCCCCACCCTCACTTCCTGACGCACAAGCTCGCTGACCA 1560
P 64	1561 1561	GAAGACCAGGAAATCCCTAGACCGAGGGGAGTTCCGCCTTCTGCATTATGCTGGAGAGGT 1620
? ;	n i	10010000000000000000000000000000000000
Db 45	1621	GACCTACAGTGTGACTGGGTTTCTGGATAAAAACAATGACTCCTCTTTCCGGAACCTGAA 1680 GACCTACAGTGTGACTGGGTTTCTGGATAAAAACAATGACCTCCTCTTCCGGAACCTGAA 1680
Qy	1681	AGTGAGCT 1740
Db	1681	GGAGACCATGTGCAGCTCAATGAACCCCATCATGGCCCAGTGCTTTGACAAGAGTGAGCT 1740
Q	1741	CAGTGACAAGAAGCGGCCAG-GACGGTGGCCACCCAGTTCAAGATGAGCCTCCTGCAGCT 1799
망	1741	CAGTGACAAGAAGCGGCCAGAGTGGCCACCCAGTTCAAGATGAGCCTCCTGCAGCT 1800
Qy	1800	CGTGGAGATCCTGAGGTCTAAGGAGCCTGCCTATATCCGGTGCATCAAGCCAAACGACGC 1859
Ъ	1801	CGTGGAGATCCTGAGGTCTAAGGAGCCTGCCTATATCCGGTGCATCAAGCCAAACGACGC 1860
Qy	1860	CAAGCAGCCGGGTCGCTTTGATGAGGTGCTCATCCGACATCAGGTGAAGTACCTGGGACT 1919
дЬ	1861	CAAGCAGCCGGGTCGCTTTGATGAGGTGCTCATCCGACATCAGGTGAAGTACCTGGGACT 1920
B 6	1920 1921	GATGGAGAATCTGCGCGTGCGCAGAGCTGGCTFTGCCTATCGTCGCAAATATGAGGCTTT 1979 
Qy	1980	CCTGCAGAGGTACAAGTCACTGTGCCCAGAGACATGGCCCCATGTGGGCCAGGACGGCCCCA 2039
Ъ	1981	CCTGCAGAGGTACAAGTCACTGTGCCCAGAGACATGGCCCCATGTGGGCAGGACGGCCCCA 2040
Qy	2040	GGATGGTGTGGCCGTGTTGGTCAGACACCTCGGCTACAAGCCAGAAGAGTACAAAATGGG 2099
Db	2041	GGATGGTGTGGCCGTGTTGGTCAGACACCTCGGCTACAAGCCCAGAAGAGTACAAAATGGG 2100
. 9	2100	CAGGACTAAGATCTTCATCCGATTCCCCAAGACCTTATTTGCCACAGAGGACTCCCTGGA 2159
ф		N
Qy	سب	AGTCCGGCGGCAGAGTCTAGCCACCAAGATCCAGGCGGCCTGGAGGGGCCTTTCATTGGCC 2219
Db	-	AGTCCGGCGGCAGAGTCTAGCCACCAAGATCCAGGCGGCCTGGAGGGGCTTTCATTGGCG 2220
, Q	22	ACAGAAATTTCTCCGGGTGAAGCGATCAGCCATCTGTATCCAGTCATGGTGGCGTGGCAC 2279
מט		N.
Qy	N	ACTGGGCCGGAGGAAGGCAAGAGGAAGTGGGCAGCCCAGACCATCCGTCGACTCAT 2339
Db	2281	ACTGGGCCGGAGGAAGGCCAAGAGGCAGCCCAGACCATCCGTCGACTCAT 2340
Q Q	2340	(.)
	, ,	4
D Q	2400	CGTGCGCGCCTCATTTTTGCTTAACCTGAGGCGGCAACTGCCCCGGAATGTTCTGGACAC
Qy	4	CTGCCCTGAGAGAGGCCTCAGAACTGCTACGGGAACTGTG 251
В	2461	5
Qy	2520	CATGAAGAACATGGTGTGGAAGTACTGCCGGAGCATCAGCCCTGAGTGGAAGCAGCAGCT 2579
В	2521	CATGAAGAACATGGTGTGGAAGTACTGCCGGAGCATCAGCCCTGAGTGGAAGCAGCAGCAGCT 2580
Qy	2580	GCAGCAAAAGGCGGTGGCTAGTGAAATTTTCAAGGGCAAGAAGGACAACTACCCCCCAGAG 2639
Db	2581	GCAGCAAAAGGCGGTGGCTAGTGAAATTTTCAAGGGCAAGAAGGACCAACTACCCCCAGAG 2640

	C 3661	3661	Db
	C 3660	3660	Qy
3660	TAG		Db
3659	TCTTGGCCAACCCTTCCTTATTCCCTTGTCTGCCTGTCCATCCA		Qy
3600	GCCTCGAACAGGGCAAGGAATGTAACTGAAAGACTGACTG	3541	Db
3599	CCTCGAACAGGGCAAGGAATGTAACTGAAAGACTGACTGGGCTGGGCTGGAAGGTCC	3540	Qy
3540	TTTTTAAGAAAGCCA	3481	da
3539	AACTATTTTTTAAGAAAGCCATTTTCCTACCCTAAACACACTGGATGTGTTTTTCCC	3480	Qy
3480	TATCTAAGACAAGGGAATTTTAACTGAGGTTTTCTCTGAGATTTTTTGATGCTTTATAGG	3421	Db
3479	ATCTAAGACAAGGGAATTTTAACTGAGGTTTTCTCTGAGATTTTTTGATGCTTTATAG	3420	Qy
3420	ACACCAATAGAAAAGCAGAGGCCTG	3361	DЬ
3419	CACACCAATAGAAAAGCAGAGGCCTGAGCCAGGCCAGGC	3360	Qy
3360	TCGCCCCTCTTGAGGTGATCAGGAGCCAGGGAGCTACCCCATGAGTGGGCCAGGCCGGG	3301	DЬ
3359	CGCCCCTCTTGAGGTGATCAGGAGCCAGGGAGCTACCCCATGAGTGGGCCAGGCC	3300	Qy
3300	CTTCCAAACAGGGATCCATGGACACCCTCAAAACCCACGCTGCAAACTCCTGCCTTCTGC	3241	DЪ
3299	TTCCAAACAGGGATCCATGGACACCCTCAAAACCCACGCTGCAAACTCCTGCCTTCTG	3240	Qy
3240	TCCTGACTCCTGATGCTTCCCTTAGTCCCCTCCCTCCCGACTTACCAAAAACTCAAG	3181	Db
3239	CCTGACTCCTGATGCTTCCCTTAGTCCCCTCCTCCCCTCCGACTTACCAAAAACTC	3180	Qy
3180	CACCTGGCTGTGGTGGCCCCACGGCTGAATTCTCGGTGATGAAGGCTGCGGTGGACCGC	3121	Db
3179	CACCTGGCTGTGGTGGCCCCACGGCTGAATTCTCGGTGATGAAGGCTGCGGTGGACCG	3120	Qy
3120	GACGGCATCATTGACTTCACATCGGGCTCAGAGCTTCTCATCACCAAGGCTAAGAATGG	3061	рь
3119	GACGGCATCATTGACTTCACATCGGGCTCAGAGCTTCTCATCACCAAGGCTAAGAATG	3060	Qy
3060	CCGCGTGAACATATCAACATCAACCAGGCAGCATAACGTTTGCAGGGGGTCCAGGCAG	3001	рь
3059	CGCGTGAACAATATCAACATCAACCAGGGCAGCATAACGTTTGCAGGGGGTCCAGGC	3000	Qy
3000	TGTGGTGCTGCAGAGTGATCGATCGAGCAGACACTAACCAAGACGGCCCTCAGTGCTGA	2941	Db
2999	GTGGTGCTGCAGAGTGATCATGTGATCGAGACACTAACCAAGACGGCCCTCAGTGCTG	2940	Qy
2940	CCTGAGTGATAGCCTATTTGTGCTTCACGTGCAGCGTGAAGACAACAACAAGCAGAAGGGAGA	2881	Db
2939	CTGAGTGATAGCCTATTTGTGCTTCACGTGCAGCGTGAAGACAACAAGCAGAAGGGAG	2880	Qy
2880	GATGCTAAAGTCAAGCAGAGAATTGATTATGCCAACCTAACCGGAATCTCTGTCAGTAG	2821	Db
2879	GATGCTAAAGTCAAGCAGAGAATTGATTATGCCAACCTAACCGGAATCTCTGTCAGTA	2820	Оу
2820	GGTTTACAAGCCTCGCCCCCGGCAGCTGCTGCTCACGCCCAGTGCTGTGGTCATTGTGGA	2761	Db
2819	GGTTACAAGCCTCGCCCCCGGCAGCTGCTGCTCACGCCCAGTGCTGTGGTCATTGTGG	2760	Qу
2760	TCAATCCTTGGGCTCTGAACCCATCCAGTATGCCGTGCCCGTGGTAAAATACGACCGTAA	2701	Db
2759	CAATCCTTGGGCTCTGAACCCATCCAGTATGCCGTGCCCGTGGTAAAATACGACCGTA	2700	Qy
2700	TGTCCCCAGACTCTTCATTAGCACACGCCTTGGCACAGAGGAGATCAGCCCCAGAGTGCT	2641	дb
2699	GTCCCCAGACTCTTCATTAGCACACGGCTTGGCACAGAGGAGAGCACCCCCAGAGTGC	2640	Qy

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: MGC Project URL: http://mgc.nci.nih.gov
Email: Gggpbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
DNA Library Preparation: Life Technologies, Inc.
Sequencing by: Mational Institutes of Health Intramural
Gathersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Mkhter, N. Ayale, K. Bockstrom-Sternberg, S.M., Benjamin, B.
Harsen, N., Ho, S.-L., Karlins, E. Kwong, Y. Haghighi, P.
Maduro, O.L., Maslelo, C., Maskeri, B., Mastrian, S. D., McCloskey, J. C.,
Tsurgeon, C., Vogt, J.L., Malker, M.A., Methersburg, N. Gupt, J. L., Granite, S. Gupt, J. Laric, P., Legaspi, R.,
Tsurgeon, C., Vogt, J.L., Malker, M.A., Wetherby, K.D., McCloskey, J.C.,
Walker, M., Zhang, L.-H. and Green, E.D. Wetherby, K.D., Wiggins, L.,
                                                                                                                                                                                                                                                                                                                                             Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. ConsortLim/LINL at: http://image.llnl.gov This clone was selected for full length sequencing because it Location/Qualifiers criteria: matched mRNA gi: 6678985.
          Direct Submission

Submitted (14 JAN-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, Mational Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 5227)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BC021481
Mus musculus, myosin I
complete cds
BC021481
TOFKWSLLQLVETLRSKEPAYIRCIKPNDAKOPGREDEVLIRHQVKYLGLMENLRVRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BC021481.1 GI:18204813
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CDS

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96.8%; Score 35/12 6	EAFLQRYKS EDSLEVRRO; QTIRRLIRGI ASELLRELCN GTEEISPRV GTEEISPRV IDYANLTGIS INQGSITFA 1444 g
3540	LCPETWPMW SLATKIQAA FILRHSPRC 4KNMVWKYC: **UQSLGSEP: *VVSSLSDSLI GGPGRDGII
	AGRPQDGVA WRGFHWRQK PENAFFLDH RSISPEWKQ IQYAVPVVK FVLHVQREDI IDFTSGSELI
	VLVRHLGYF FLRVKRSAI VRASFLLNL QLQQKAVAS VDRKGYKPR VRQKGDVVLA
	(PEEYKMGR?) (CIQSWWRGT) RRQLPRNVL EIFKGKKDN PRQLLLTPS OSDHVIETL CAVVAPRLN(
	'KIFI 'LGRR DTSW YPQS AVVI AVVI IKTA IRTA

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882 TCAGCATCGTGGCCAGCGTCGTACATCTGGGCAACATCCACTTTGCTGCTGACGAGGACA 941 762 TGTACCTGGTGAAGGGCCAGTGTGCCAAGGTCTCCTCCATCAACGACAAGAGTGACTGGA 821 757 AGGGGGGCGAGGAGAGTCTCCGTCGGCTGGGCTTGGAACGGAACCCCCAGAGCTACT 816 697 CCCGGGTGGTGCACCAAAATCACGGAGAGCGGGAACTTCCACGTCTTTTACCAGCTACTGG 642 CCCGGGTGGTGCACCAAAATCACGGAGGGGGAACTTCCACGTCTTTTACCAGCTACTGG 522 GGAATGCCAAGACTCTCCGCCAACGATAACTCCAGCCGGTTTGGAAAGTACATGGATGTGC 581 517 AACGGGGTGGCGCAGTGCGAGACCGCCTGTTGCAGAGCAACCCCCGTGTTAGAGGGCCTTTG 576 AGGTTATGAGGAAGGCGCTGTCCGTCATTGACTTCACTGAGGATGAAGTGGAGGACTTGC AGGTTÁTGAGGAAGGCGCTGTCGTCATTGACTTCACTGAGGATGAAGTGGÁGGACTTGC 936 457 GGAAGACAGAGGGCCACCAAGAGACACTGCTCCAGTTCTATGCAGAGACCCTGCCCAGCCCCTG Matches 3590; TĠŦAĊĊŦĠĠŦĠĀĀĠĠĠĊĊĀĠŦĠŦĠĊĊĀĀĠĠŦĊŦĊĊŤĊĊĀŦĊĀĀĊĠĀĊĀĀĠĀĠŦĠĀĊŦĠĠĀ 337 GrégréreAgriréraréaagraceaecréartrertrecagrégeréaeaecaergrafia AGGGGGCGAGGAGGACTCTCCGTCGGCTGGGCTTGGAACGGAACCCCCAGAGCTACT 761 282 GTGGTGTCAGTTTCTATGAAGTACCACCTCATTTGTTTGCAGTGGCTGACACTGTATACC AGTTTGACTTCAAGGGTGCCCCCGTGGGAGGCCACATTCTCAGTTACCTCCTGGAAAAGT 641 217 ÁGAACCTCCGGCGGCGGGTTCCGGGGAGAACCTTCATTTATACCTACATCGGTCCTGTCCTAG 162 AGAACCTCGGGGGGGTTCCGGGAGAACCTCATTTATACCTACATCGGTCCTGTCCTAG GGAATGCCAAGACTCTCCGCAACGATAACTCCAGCCGGTTTGGAAAGTACATGGATGTGC 636 157 GGTAGGGGTGCAGGACTTTGTCCTGCTGGAGAATTTCACCAGTGAGGCTGCCTTCATTG 102 GGGTAGGGGTGCAGGACTTTGTCCTGCTGGAGAATTTCACCAGTGAGGCTGCCTTCATTG AACGGGTGGCGCAGTGCGAGACCGCCTGTTGCAGAGCAACCCCGTGTTAGAGGCCTTTG 521 GCAAGACAGAGGCCACCAAGAGACTGCTCCAGTTCTATGCAGAGCTGCCCAGCCCCTG 461 Conservative 99.38; 0; Pred. No. 0; Mismatches DB 10; Length 5227; 876 701 341 336 276 281 221 216 161

ОУ	942	GCAATGCCCAGGTTACTACTGAGAACCAGCTCAAATATCTGACCAGGCTCCTTGGTGTGG 10	01
В		TACTGAGAACCAGCTCAAATATCTGACCAGGCT	56
3 8	1002	AAGGTACAACACTTAGGGAAGCCCTGACCCACAGGAAGATCATCGCCAAGGGGAAGAGGC 10	61
Qy	90	CTGAGCCCACTGAACCTTGAACAGGCGGCATATGCAAGGGATGCGCTTGCCAAGGCTG 1	
Вþ	1117	TCCTGAGCCCACTGAACCTTGAACAGGCGGCATATGCAAGGGATGCGCTTGCCAAGGCTG 11	76
Qy	1122	TGTACAGCCGGACATTCACCTGGCTGGCTCAGAAAGATCAATAGGTCACTGGCCTCTAAGG 11	82
DЬ	1177	AGCCGGACATTCACCTGGCTGGTCAGAAAGATCAATAGGTCACTGGCC	36
B 8	1182	ACGCTGAGAGCCCCAGCTGGCGAAGCACCACGGTTCTTGGGCTCCTGGACATTTACGGCT 12	41
Ş	24	AGTGTTTCAGCATAACAGCTTTCGAGCAGTTCTGCATCAACTACTACTACTAATGAGAAGC	0 1
Db .	9	NIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	ÇT (
Qγ		3CAGCTCTTCATCGAGCTGACTCTCAAGTCGGAGCAGGAGGAATACGAGGCTGAGG	61
Ъ	1357	GCAGCTCTTCATCGAGCTGACTCTCAAGTCGGAGCAGGAGG	16
29	w	GCATCGCGTGGGAACCTGTCCAGTACTTCAACAACAACATCATCTGTGAGCTGGTAGAGG 14	2
	;	**************************************	,
Db	1477	CGTCCTGGGGAGGCCA	36 F
Qy		GGACCTGACCTTTCTGGAGAAGTTGGAGGACACTGTCAAGCCCCACCCTCACTTCCTG	41
DЬ	1537	CGGACCTGACCTTTCTGGAGAAGTTGGAGGACACTGTCAAGCCCCACCCTCACTTCCTGA 15	96
Qy	1542	CGCACAAGCTCGCTGACCAGAAGACCAGGAAATCCCCTAGACCGAGGGGAGTTCCGCCTTC 16	
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Qy	Ν		61
DЬ	657	TGACCTACAGTGTGACTG	16
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20	1	CCTCTTCCGGAACCTGAAGGAGACCATGTGCAGCTCAATGAACCCCCATCATGGCCCAGT 1	76
P 04	1722	GCTTTGACAAGAGTGAGCTCAGTGACAAGAAGCGGCCAG-GACGGTGGCCACCCAGTTCA 17	, e
δÃ	7	GATGAGCCTCCTGCAGCTCGTGGAGATCCTGAGGTCTAAGGAGCCTGCCT	4
Db	1837	AGATGAGCCTCCTGCAGCTCGTGGAGATCCTGAGGTCTAAGGAGCCTGCCT	96
Qy	1841	GCATCAAGCCAAACGACGCCAAGCAGCCGGGTCGCTTTGATGAGGTGCTCATCCGACATC 19	00
Db	1897	ATCAAGCCAAACGACGCCAAGCAGCCGGGTCGCTTTGATGAGGTGCTCATCCC	56
Qy	Ō	AGGTGAAGTACCTGGGACTGATGGAGAATCTGCGCGTGCGCAGAGCTGGCTTTGCCTATC 19	60
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Qy	1961	GTCGCAAATATGAGGCTTTCCTGCAGAGGTACAAGTCACTGTGCCCAGAGACACTGGCCCA 20	N
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3036	ACAACAAGCAGAAGGAATGTIGGTIGCTGCAGAGTGATCATGTIGATCGAGACACTAACCA	2977	מם עע
9	CGGAATCTCTGTCAGTAGCCTGAGTGATAGCCTATTTGTGCTTCACGTGCAGCGTGAA	9 1	20
92	CCGGAATCTCTGTCAGTAGCCTGAGTGATAGCCTATTTGTGCTTCACGTGCAGCGTGAAG	2861	y Qy
2916	GTGCTGTGGTCATTGTGGAGGATGCTAAAGTCAAGCAGAGAATTGATTATGCCAACCTAA	2857	Db
2860	TGCTGTGGTCATTGTGGAGGATGCTAAAGTCAAGCAGAGAATTGATTATGCCAACCTA	2801	Qy
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2616	ACTGCTACGGGAACTGTGCATGAAGAACATGGTGTGGAAGTACTGCCGGAGCATCAGCC	2557	Db
2560	CTGCTACGGGAACTGTGCATGAAGAACATGGTGTGGAAGTACTGCCGGAGCATCAGC		Оу
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2500	CCGGAATGTTCTGGACACCTCCTGGCCCACACCCCCCACCTGCCCTGAGAGAGGCCTCA	2441	УО
2496	ATGCCTTCTTGGACCACGTGCGCGCCTCATTTTGCTTAACCTGAGGCGGCAACTGC	2437	Db
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		w	Дb
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2140	RGAAGAGTACAAAATGGGCAGGACTAAGATCTTCATCCGATTCCCCAAGACCTT	2081	Qy
Ë		07	DЬ
2080	GTGGGCAGGACGGCCCCAGGATGGTGTGGCCGTGTTGGTCAGACACCTCGGCTACAAG	2021	γQ

3157 TCACCAAGGCTAAGAATGGCCACCTGGCTGTGGTGGCCCCACGGCTGAATTCTCGGTGAT

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3581 GCTGGGCTGGAAGGTCCTCTTCT-TGGCCAACCCTTCCTTATTCCCTTGTCTGTCTGTCC 3639
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3461 TTTTTTGATGCTTTATAGGAAACTATTTTTTTAAGAAAGCCATTTTCCTACCCTAAACAC 3520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3341 ATGAGTGGGCCAGGCCGGGCCACACCAATAGAAAGCAGAGGCCTGAGCAGGCCAGGGCA 3400
3396 ATGAGTGGGCCAGGCCGGGCCACAGGAATAGAAAGCAGAGGCCTGAGCAGGCCAGGCCA 3400
3455
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Ruppert C., Godel, J., Reinhard, J. and Ba
WR-2 a novel class-I Myosin identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3221 GACTTACCAAAAACTCAAGCTTCCAAACAGGGATCCATGGACACCCTCAAAACCCACGCT 3280
3277 CAGTTACCAAAGCTCAAGCCTTCCAGACAGGGATCCATGGACACCCTCAAAACCCACGCT 3280
3278 GAGTTACCAAAGACTCAAGCTTCCAGACAGGGATCCATGGACACCCTCAAAACCCAC-CT 3335
                                                                                                                                                                            Ruppert.C.
Ruppert.C.
Direct Submission
Submitted (26-AUG-1993) C. Ruppert, Friedrich-Miescher-Laboratorium
                                                                                                                                                                                                                                              RNMYR2
R. norvegicus MYR2 mRNA for myosin I heavy chain.

X74800 1 GI:400428
MY82 mY82 gene.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Rattus is Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Rattus norvegicus"
/strain="sprague-Dawley"
/bb_xref="taxon:10116"
/clone_lib="MII5'-2,35-1,x338"
/dev_stage="adult"
267. .3353
                                                                                                                                                                    Baehler, M
                                                                                                                                                          in rat brain
                                                                                                                                                                                                                                                                                                                    ROD 22-SEP-1993
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794 CCCTGTGGGAGGCCACATTCTCAGTTACCTCCTGGAGAAGTCTCGAGTGGTACACCAGAA
        601 CCCCGTGGGAGGCCACATTCTCAGTTACCTCCTGGAAAAGTCCCCGGGTGGTGCACCAAAA 660
                                   734 CAACGACAACTCCAGCCGCTTTGGGAAGTACATGGATGTGCAGTTTGACTTCAAGGGTGC
                                            541 CAACGATAACTCCAGCCGGTTTGGAAAGTACATGGATGTGCAGTTTGACTTCAAGGGTGC 600
                                                                       674 AGACCCCCTGTTGGAGAGCAACCCTGTGCTGGAGGCCCTTTGGGAATGCCAAGACTCTCCG
                                                                               481 AGACCGCCTGTTGCAGAGCAACCCCGTGTTAGAGGCCTTTGGGAATGCCAAGACTCTCCG 540
                                                                                                          BASE COUNT
ORIGIN
                                                                                                                                              554 TCGGGACCAAGCAGTGATGATTTCTGGAGACAGTGGGGCAGGGAAGACAGAGGCCACCAA 613
                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                             301 AGTACCACCTCATTTGCTTTGCAGTGGCTGACACTGTATACCGGGCACTTCGTACTGAGCG 360
                                                                                                                                                                                                                     374 CCGGGAGAACCTCATTTATACCTACATTGGCCCTGTCCTGTCTCTGTCAACCCCTACCG 433
                                                                                                                                                                                                                                                                    314 TGTTCTCCTGGAGAACTTCACCAGTGAGGCTGCCTTCATTGAGAACCTCCGGCGTCGATT 373
                                                                                                                                                                                                                                                                                                        121 TGTCCTGCTGGAGAATTTCACCAGTGAGGCTGCCTTCATTGAGAACCTCCGGCGGCGGTT 180
                                                                                                                                                                                                                                                                                                                                  254 GETACGAGTGACCATGGAGAGGGCCTTGACTGCCCGAGACCGGGTGGGGGTGGAAGACTT
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                                                                                                                                                                                  AGTGCCGCCTCATCTGTTTGCAGTGGCTGACACTGTATACCGGGCGCTTCGTACTGAGCG 553
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                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="myosin I heavy chain"
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                                                                                                                                                                                                                                                                                                                                                                                                                   88.3%; Score 3232.8; DB 10; Length 3810;
                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches 182; Indels
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5

FCATURES SOURCE

Location/Qualifiers

CDS

/gene="MYR 2" 267. .3353 'gene≖"MYR 2"

JOURNAL

REFERENCE AUTHORS TITLE

REFERENCE AUTHORS TITLE

JOURNAL

KEYWORDS SOURCE

ORGANISM

RESULT 3
RNMYR2
LOCUS
DEFINITION
ACCESSION
VERSION VERSION

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1933	GGAGACCATGTGCAGCTCCACGAACCCCATCATGCCCAGTGCTTTGACAAGAGTGAGCT	1874	B 4
87	ACCTACAGCGTGACTGGGTTTCTGGATAAAAACAATGACCTCCTCTTCCGGAACCTGA	3 2	) Db
68	GACCTACAGTGTGACTGGGTTTCTGGATAAAAAACAATGACCTCCTCTTCCCGGAACCTGAA	62	, Q
1813	HILLIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHI	75	D 5
ა თ	CTGGAGGACACAATCAAGCACCCTCACTTCCTGACGCACAAGCTTGCTGACC	1694	\$ B
	GAAGTTGGAGGACACTGTCAAGCCCCACCCTCACTTCCTGACGCACAAGCTCGCTGACCA	50	Ş
1500 1693	CTCCATCTTGAATGAAGAGTGCCTGCGTCCTGGGGAGGCCACGGACCTGACCTTTCTGGA	1634	Дb
63	CTTCAACAACAAGATCATCTGTGACCTGGTGGAGGAGAAATTCAAGGGCATCAT	· u	рb
	CCAGTACTTCAACAACAAGATCATCTGTGACCTGGTAGAGGAGAAGTTCAAGGGCATCAT	1381	Qy
1573	GCTGACTCTCAAGTCCGAGCAGGAGGAATACGAGGCAGAGGGCATCGCGTGGGAACCTGT	1514	Db
1380	TCTCAAGTCGGAGCAGGAAGAGAATACGAGGCTGAGGGCATCGCGTGGGAACCTG	w	Qy
1513	CAGCTTCGAGCAGTTCTGCATCAACTATTGCAATGAGAAGCTGCAGCAGCTCTTCATTGA	1454	B 4
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. 26	GCGAAGCACCACGGTTCTTGGGCTCCTGGACATTTACGGCTTTGAAGTGTTTCAGCATAA	20	} Q
1393	G -		рь
1200	TGGTCAGAAAGATCAATAGGTCACTGGCCTCTAAGGACGCTGAGAGCCCCAGCT	$\vdash$	Qу
1140 1333	TGAACAGGCGGCATATGCAAGGGATGCGCTTGCCAAGGCTGTACAGCCGGACATTCAC	1081 1274	Db Oy
1273	CCTGACCCACAGGAAGATCATCGCCAAGGGGGAAGAGCTCCTGAGCCCACTGAACCT	N	рь
1080	CACAGGAAGATCATCGCCAAGGGGGAAGAGCTCCTGAGCCCCACTGAACC	1021	Qy
1213	TGAGAACCAGCTCAAATATCTGACCAGGCTCCTTGGTGTGGAAGGCACAACACTGAGGGA		Ъ
1020	ACCAGCTCAAATATCTGACCAGGCTCCTTGGTGTGGAAGGTACAACACTTAGGG	961	Qy
960 1153	CCTACATCTGGGCAACATCCACTTTGCTGCTGACGAGGACAGCAATGCCCAGGTTACTAC	901	Db Qy
	TCATTGACTTCACTGAGGATGAAGTGGAGGACTTGCTAAGCATCGTGGCCAGCGT	ū	Db
900	GTCCGTCATTGACTTCACTGAGGATGAAGTGGAGGACTTGCTCAGCATCGTGGCCAGCGT	841	οy
1033	GTGTGCCAAGGTCTCCTCCATCAATGACAAGAGTGACTGGAAGGTTGTGAGGAAGGCGCT	974	рь
840	CCAAGGTCTCCTCCATCAACGACAAGAGTGACTGGAAGGTTATGAGGAAGGCGCT	781	Qy
780 973	TCTCCGTCGGCTGGGCTTGGAACGGAACCCCCAGAGCTACTTGTACCTGGTGAAGGGCCA	721 914	Db Qy
913	GAGAACGGAACTTCCACGTCTTTTACCAGCTCCTGGAGGGGGGGG		DЬ
720	GAACTTCCACGTCTTTAACCAGCTACTGGAGGGGGGGCGAGGAGGAGAC	661	Qy

2879	$\tt GGATGCTAAAGTCAAGCAGAGAATTGATTATGCCAACCTAACCGGAATCTCTGTCAGTAG$	2820	Qy
3013	GGCCTACAAGCCTCGTTCCCGGCAGCTGCTGCTCACACCCCAGTGCTGTGGTCATCGTGGA	2954	dα
2819	GGTTACAAGCCTCGCCCCCGGCAGCTGCTGCTCACGCCCAGTGCTGTGGTCATTGTGG	2760	Qy
2953	CCTTGGGCTCTGAACCCATCCAGTATGCAGTGCCTGTGGTAAAATACGACCG	2894	рь
2759	CAATCCTTGGGCTCTGAACCCATCCAGTATGCCGTGCCCGTGGTAAAATACGACCGT	2700	Qy
2893	TGTCCCCAGACTTTTCATCAGCACACGCCTTGGCACAGAGGAGTCAGCCCCCAGAGTGCT	2834	Db
2699	GTCCCCAGACTCTTCATTAGCACACGGCTTGGCACAGAGGAGATCAGCCCCAGAGTG	2640	Qy
2833	GCAGCAAAAGGCGGTGGCTAGTGAAATTTTCAAGGGCAAGAAGGACAATTACCCCCAGAG	2774	Db
2639	CAGCAAAAGGCGGTGGCTAGTGAAATTTTTCAAGGGCAAGAAGGACAACTACCCCCAGA	2580	Qy
77		71	Db .
2579	TGAAGAACATGGTGTGGAAGTACTGCCGGAGCATCAGCCCTGAGTGGAAGCAGC	2520	Qy
2713	CTCCTGGCCCACACCCCGACCTGCCCTGAGAGAGGCCTCGGAGCTGCTCCGGGAGCTATG	2654	Db
2519	CCTGGCCCACACCCCCACCTGCCCCTGAGAGGGCCTCAGAACTGCTACGGGAAC	2460	Qy
2653	CGTGCGCACGTCATTTTTGCTTAACCTGAGGCGACAACTACCCCGGAATGTTCTGGACAC	2594	Db
2459	GTGCGCGCCTCATTTTTGCTTAACCTGAGGCGGCAACTGCCCCGGAATGTTCTGGAC	2400	Qy
2593	CGTGGCTTCATTTTGCGTCATGCACCCCGGTGCCCTGAGAATGCCTTCTTCCTGGACCA	2534	Db
2399	CGTGGCTTCATTTTGCGCCATTCACCCCGGTGCCCTGAGAATGCCTTCTTCTTGGACC	2340	Qy
2533	ACTGGGCCGGAGGAAGGCAAAAAGGAAGTGGGCAGCCCAGACTATCCGTAGACTCAT	2474	Дb
2339	CTGGGCCGGAGGAAGGCAGCCAAGAGGAAGTGGGCAGCCAGACCATCCGTCGACTC	2280	Qy
2473	GCAGAAAFTTCTCCGGGTGAAGCGATCAGCCATCTGTATCCAGTCCTGGTGGCGCGGTAC	2414	Db
2279	AGAAATTTCTCCGGGTGAAGCGATCAGCCATCTGTATCCAGTCATGGTGGCGTGGC	2220	Qy
2413	AGTCCGACGGCAGGTCTAGCCCACCAAGATCCAGGCGGCGTGGAGGGGGCTTTCATTGGCG	2354	Db
2219	GTCCGGCGGCAGAGTCTAGCCACCAAGATCCAGGCGGCCTGGAAGGGGCTTTCATTGGC	2160	Qy
2353	CAGGACTAAGATCTTCATCCCGATTCCCCCAAGACCTTGTTTGCCACAGAGAGCTCCCTGGA	2294	дb
2159	AGGACTAAGATCTTCATCCGATTCCCCAAGACCTTATTTGCCACAGAGGACTCCCTG	2100	Qy
2293	GATGGGGTGGCTGTGTTGGTCAGACACCTTGGCTATAAGCCAGAAGAGTACAAAATGGG	2234	рb
2099	GATGGTGTGGCCGTGTTGGTCAGACACCTCGGCTACAAGCCAGAAGAGTACAAAATG	0	Qy
w	CCTGCAGAGGTACAAGTCACTGTGCCCAGAGACATGGCCCGTGTGGACAAGACGGCCCCA		DЬ
2039	CTGCAGAGGTACAAGTCACTGTGCCCAGAGACATGGCCCATGTGGGCAGGACGGCCCC	1980	Оу
2173	TATGGAGAATCTGCGTGTGCGCAGAGCTGGCTTTGCCTACCGTCGAAAATATGAGGCTTT	2114	Db
1979	GGAGAATCTGCGCGTGCGCAGAGCTGGCTTTGCCTATCGTCGCAAATATGAGGC	1920	Qy
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2053	AGTGGAGATCCTGAGGTCTAAGGAACCTGCTTATATCCGGTGCATCAAGCCAAATGACGC	1994	Db
1859	TGGAGATCCTGAGGTCTAAGGAGCCTGCCTATATCCGGTGCATCAAGCCAAACGACG	1800	γQ
99	് ~-	.93	Db
1799	AGTGACAAGAAGCGGCCAG-GACGGTGGCCACCCAGTTCAAGATGAGCCTCCTGCAGC	1741	Qy

REFERENCE AUTHORS Hamille: Rutherla; Rodentia; Craniata; Vertebrata; Euteleostomi; to 311] Hamilton, B.A., Smith, D.J., Mueller, K.L., Kerrebrock, A.W., Memhauser, J.L., Hawkins, T.L., Baly, M.J., Kruglyak, L., Reeve, M.P., expression of PTPp alpha: Positional Complementation via reduced 97325785  PUBMED 9182797	Db 3014 GIIII
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BASE COUNT	CDS	REFERENCE AUTHORS TITLE JOURNAL FEATURES SOURCE	ORGANIS FERENCE AUTHORS TITLE OURNAL EDLINE PUBMED	RESULT 5 HSMYOIB LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE	Db 2881 Oy 3002 Db 2941 Oy 3062 Db 3001 Oy 3122 Db 3061
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Qу	Db Qy	Оy	Оy	Qу		ОУ	Db	Qγ	Qу Db	Qу	Db Qy	ор	dg dy	рь	dd dy	Db VY	B 4	OV
2081 CAGAAGAGTACAAAATGGGCAGGACTAAGATCTTCATCCGCATTCCCCAAGACCTTATTTG 2140	2021 TGTGGGCAGGACGCCCCAGGATGGTGGCCGTGTTGGTCAGACACCTCGGCTACAAGC 2080	961 954	01 94	GCATCAAGCCAAAGGAGCCAAGCAGCGGGTGCTTTGATGAGGTGCTCATCCGACATC	4 1	1722 GCTTTGACAAGAGTGAGCAGTGACAAGAAGCGGCCAG-GACGGTGGCCAGCCAGTTCA 1780	1652 TCCTCTTCCGGAACCTGAAGGACCATGTGCAGCTCAATGAACCCCATCATGCCCCAGT 1721 1654 TTCTCTTCCGGAACCTTAAGGAGACCATGTGTAGCTCAAAGAATCCCATTATGAGCCCAGT 1713	2 TGCATTATIGCTGGAGAGGTGACCTACAGTTTGGGTTTTCTGGATAAAAACAATGACC 	2 CGCACAAGCTCGCTGACCAGAAGACCAGGAAATCCCTAGACCGAGGGGAGTTCCGCCTTC 	2 GGACCTGACCTTTCTGGAGAAGTTGGAGGACACTGTCAAGCCCCACCCTCACTTCCTGA	2 AGAAGTICAAGGCATICATCICCATCTIGGATGAAGAGTIGCCTGCGGGGGGAGGCCA	2 GCATIGGGTGGGAACCTGTCCAGTACTTCAACAACAAGATCATCTGTGACCTGGTAGAGG	2 TGCAGCAGCTCTTCATCGAGCTGACTCTCAAGTCGGAGCAGGAGGAATACGAGGCTGAGG	1242 TIGAAGIGTTTCAGCATAACAGCTTCGAGCAGTTCIGCATCACTACTGCAATCAGAAGC 1301	ACGTGARAGCCCCAGCTGGCGARGCACCACGGTTCTTGGGCTCCTGGACATTTACGGCT	TOTACHOCUSEC AT LONG LEGAL CONTROL C		1062 TCCTGAGCCCACTGAACCTTGAACAGGCGGCATATGCAAGGGATGCGCTTGCCAAGGCTG 1121

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3221 GACTTAGCAAAAACTCAAGCTTCCAAACAGGGATCCATGGACACCCTCAAAACCCACGCT 3280
                                          3154 AAAGGCGCCACTGGACCATCCCAACGCCCAAAGCTTTGCTTTTCTCCTCCTCCCTTCC
                                                               3101 TCACCAAGGCTAAGAATGGCCACCTGGCTGGTGGTGGCCCCACGGCTGAATTCTCGGTGAT 3160
                                                                                                                                                     3041 TTGCAGGGGGTCCAGGGAGGGACGGCATCATTGACTTCACATCGGGCTCAGAGCTTCTCA 3100
3034 TTGCAGGGGGCCCCGGCAGGGATGGCATCACTTCACATCGGGCTCAGAGCTTCTCA 3100
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2914 ACATAAAGCAAAAGGGAGATGTGGTGGTGCTGCAGAGTGATCAAGCA 2980
2916 ACATAAAGCAAAAGGGAGATGTGGTGGTGCTGCAGAGTGACCACGTGATTGAGACGCTGACCA 2973
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2734 TTGTGAAATACGACCGCAAGGGCTACAAGCCTCGCTCGCCCGGCAGCTGCTGCTCACGCCCA 2800
2739 TTGTGAAATACGACCGCAAGGGCTACAAGCCTCGCTCGCCTCCCGGCAGCTGCTGCTCACGCCCA 2793
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2561 CTGAGTGGAAGCAGCAGCTGCAGCAAAAGGCGGTGGCTAGTGAAATTTTCAAGGGCAAGA 2620
                                                                                              TĈACCAAGGCCAAGAACGGGCACCTGGCTGTGGTCGCCCCCACGGCTGAATTATCGGTGAT 3153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2441 CCCGGAATGTTCTGGACACCTCCTGGCCCACACGCCCACCTGCCCTGAGAGAGGCCTCAG 2500
2434 CCCGGAATGTCCTGGACACCTACTGGCCCACCCCCCACCTGCCCTGAGAGAGGCCTCAG 2500
                                                                                                                                                                                                                                AGACGGCCCTCAGTGCTGACCGCGTGAACAATATCAACATCAACCAGGGCAGCATAACGT 3040
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2374 ACGCCTTCTTCTTGGACCATGTGCGCACGTCTTTTTGCTAAACCTGAGGCGCAACTGC 2440
2374 ACGCCTTCTTCTTGGACCATGTGCGCACGTCTTTTTTGCTAAACCTGAGGCGGCAGCTGC 2433
                                                                                                                                                                                                                AGÁCAGGGCTGAGTGCCAAGGGGTGAAGAGCATCAACATCAAGGAGGAGGATAÁGGT 3033
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                                                                                                                                                                                                                                                                                                                                  CCGGAATCTCTGTCAGCAGCCTGAGCGACAGTCTTTTTGTGCTTCATGTACAGCGTGCGG
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2134 CCACAGAGGATGCCCTTGGAGGTCCGGCGGCAGAGCCTGGCCACAAGATCCAGGCGGCCT 2200
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10/1 g 596 t	// / / / / / / / / / / / / / / / / / /	/db xref="taxon:9913" /clone==6" /clone==6" /sex="male=" /itssue_type="adrenal gland" /clone_lib="uambda gt-11, bovine adrenal gland, made by /dev_stage="adult" 1. 100 101. 3187	2 (Dases 1 to 3505) 3 (Direct Submission 3 (Dase I Submission) 4 (Dase I Sub	Bos taurus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bovidae; Botinae; Bos 1 to 3505) A novel myosin I from bovine adrenal gland FEBS Lett 339 (1-2), 31-36 (1994) 8313076 8313076		^ -	

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	10 AAGCATCGTGGCCCACCTTCTGCATCTGGGCCAACCACTTTGCCCCCAATGAGGAGAG 96 43 CAATGCCCAGGTTACTACTGAGAACCAGCTCAAATATCTGACCAAGCCTCCTTGGTGTGGA 10 111	Qy Db
	O GETGETCAGGAGGAGGACTGACTGTCATCGACTTCACCGAGGAGGAGGAGGAGGAGGACGTGGAGGACGACATCCACTTTGCTGACGACGACGACGACGACGACGACGACGACGACGACGACG	Q Y
	23 GGTTATGAGGAAGGCGCTGTCCGTCATTGACTTCACTGAGGATGAAGTGGAGGACTTGCT 8  111	P 29
	763 GTACCTGGTGAAGGGCCAGTGTGCCAAGGTCTCCCTCCATCAACGACAAGAGTGACTGGAA 822	Db Oy
	703 GGGGGGCGAGGAGACTCTCCGTCGGCTGGGCTTGGAACGGAACCCCCAGAGCTACTT 762 	Qy Db
	643 CCGGGTGGTGCACCAAAATCACGGAGAGCGGAACTTCCACGTCTTTTACCAGCTACTGGA 702 	Оу
	583 GTTTGACTTCAAGGGTGCCCCCGTGGGAGGCCACATTCTCAGTTACCTCCTGGAAAAAGTC 642	Qy Db
	523 GAATGCCAAGACTCTCCGCAACGATAACTCCAGCCGGTTTGGAAAGTACATGGATGTGCA 582	Qy Db
	463 ACGGGGTGGCGAGTGCGAGACCGCCTGTTGCAGAGCAACCCCGTGTTAGAGGCCTTTGG 522	Qy Db
	403 CAAGACAGAGGCCACCAAGAGACTGCTCCAGTTCTATGCAGAGACCTGCCCAGCCCCTGA 462 	Qy Db
	343 GGCACTTCGTACTGAGCGTCGGGACCAGGCAGTGATGATTTCTGGAGAGAGTGGGGCAGG 402 	Qy Db
	283 TGGTGTCAGTTTCTATGAAGTACCACCTCATTTGTTTGCAGTGGCTGACACTGTATACCG 342	Qy Db
	223 CTCTGTCAATCCCTACCGAGACCTACAGATCTACAGCCGGCAGCATATGGAACGCTACCG 282	Qy Db
	163 GAACCTCCGGCGGCGGTTCCGGGAGAACCTCATTTATACCTACATCGGTCCTGTCCTAGT 222	Qy Db
	103 GGTAGGGGTGCAGGACTTTGTCCTGCTGGAGAATTTCACCAGTGAGGCTGCCTTCATTGA 162 	Qy Db
	43 GGCCCTGGGCAGTGACGGGGTTCGAGTGACCATGGAGAGCGCCTTGACTGCCCGAGACCG 102 	Qy Db
80	Ouery Match 70.9%; Score 2595.2; DB 4; Length 3505; Best Local Similarity 86.3%; Pred. No. 0; Matches 2980; Conservative 0; Mismatches 458; Indels 10; Gaps	Z 20 O

CACAGAGGACTCCCTGGAAGTCCGGCGGCAGAGTCTAGCCACCAAGATCCAGGCGGCCTG 2201	2142 C	Qy
AAGAGTACAAGATGGGCAGGACCAAGA	G	Db
AGAGTACAAAATGGGCAGGACTAAGATCTTCATCCGATTCCCCAAGACCTTATTTG	2082 A	Qy
ACAGGACGCCGCCAGGATGGGGTGACTGTGCTGGTCAGGCACCTGGGCTACAAGC	2050 G	рb
TGGGCAGGACGGCCCCAGGATGGTGTGGCCGTGTTGGTCAGACACCTCGGCTACAAG	2022 G	Qy
CGCAAATACGAGGCTTTCCTGCAGAGGTACAAGTCACTGTGCCCAGAGAGACATGGCCCAC 20	990 c	Db .
AATATGAGGCTTTCCTGCAGAGGTACAACTCACTGTGCCCAGAGACATGCCCCAT 20	962 1	0
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GTGAAGTACCTGGGACTGATGGAGAATCTGCGCGTGCGCAGAGCTGGCTTTGCCTATCG 19	902 0	Qy
CATCAAGCCCAATGACTCCAAGCAGCCCGGCCGCTTTGATGAGGTGCTAATCCGGCACCA 1929	1870 C	Дb
ATCAAGCCAAACGACGCCAAGCAGCCGGGTCGCTTTGATGAGGTGCTCATCCGACATC	842 (	Qy
GATGAGCCTCCTGGAGCTGGTAGAGATCTTGAAGTCAAAGGAGCCTGCCT	1810 G	Db
ATGAGCCTCCTGCAGCTCGTGGAGATCCTGAGGTCTAAGGAGCCTGCCT	782 6	Qy
CTTCGACCGGAGTGAGCTCAGCAGCAAGAAGCGGCCAGAGACGGTGGCCACCCAGTTCAA 1809	750	. Db
TGACAAGAGTGAGCTCAGTGACAAGAAGCGGCCAGCGAGGCGACCCAGTTC	ũ	Qy
TCTCTTCCGGAACCTGAAGGACCATGTGCAGCTCGGAGAACCCCATCCTGGGCCAGTG 1749	1690 т	Db
TTCCGGAACCTGAAGGAGACCATGTGCAGCTCAATGAACCCCATCATGGCCCAC	663 (	Qy
GCACTATGCCGGGGAGGTGACCTACAACGTGACCGGGTTTCTGGATAAAAACAACGACCT 1689	30 0	Db
CATTATGCTGGAGAGGTGACCTACAGTGTGACTGGGTTTCTGGATAAAAACAATGACC	603 (	Qy
GCACAAGCTGGCTGACCAGCGGACCAGGAAATCTCTGGACCGCGGGGAGTTCCGCCTCCT 1629	1570 G	фd
AAGCTCGCTGACCAĠAAGACCAGGAAATCCCTAGACCGAGGGGAGTTCCGCCTTC	543	Qy
GGACCTGACCTTCCTGGAGAAGCTGGAGGACACAATCAAGCAGCATCCACACTTCCTGAC 1569	1510 G	Db
GACCTGACCTTTCTGGAGAAGTTGGAGGACACTGTCAAGCCCCACCCTCACTTCCTG	483 (	Qy
GAAGTTCAAAGGCATCATCTCCATTTTGGACGAGGAGTGTCTGCGTCCCGGGGAGGCCAC 1509	1450 G	ф
AAGTTCAAGGGCATCATCTCCATCTTGGATGAAGAGTGCCTGCGTCCTTGGGGAGGC	423 0	Оy
CATCGCGTGGGAACCGGTCCAGTATTTCAACAACAAGATTATCTGTGACCTGGTGGAGGA 1449	390	Дb
ATCGCGTGGGAACCTGTCCAGTACTTCAACAACAAGATCATCTGTGACCTGGTAGAGG	363 (	Qy
ACAGCAGCTCTTCATCGAGCTCACCCTCAAGTCAGAGCAGGAGGAGTATGAGGCCGAGGG 1389	330 1	Дb
CAGCTCTTCATCGAGCTGACTCTCAAGTCGGAGCAGGAGGAATACGAGGCTGAGG	03 (	Qy
TGAAGTGTTCCAGCACAACAGCTTTGAGCAGTTCTGCATCAATTACTGCAATGAGAAGCT 1329	270 T	Дb
GAAGTGTTTCAGCATAACAGCTTCGAGCAGTTCTGCATCAACTACTGCAATGAGAAGC	243 T	Qy
TGCCGAGAGCCCCAGCTGGCGAGCACCACCGTCCTCGGGCTACTGGGCATTTACGGCTT 1269	210 T	Db
CTGAGAGCCCCAGCTGGCGAAGCACCACGGTTCTTGGGCTCCTGGACATTTACGG	183 C	Qу
GTACAGTCGCACCTTTACCTGGCTGGTCGCGAAGATCAACAGGTCGCCTGGCCTCCAAGGA 1209	150	Db
ACAGCCGGACATTCACCTGGCTGGTCAGAAAGATCAATAGGTCACTGGCCTCTAAGG	23	Qy
CCTGAGCCCGCTGAACCTAGAACAGGCTGCATATGCACGGGACGCCCTCGCCAAGGCTGT 1149	090	DЪ
TGAGCCCACTGAACCTTGAACAGGCGGCATATGCAAGGGATGCGCTTGCCAAGGC	1063 C	Оу

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3221 GACTTACCAAAAACTCAAGCTTCCAAAACAGGGATCCATGGACACCCTCAAAACCCACGCT
                                                    3162 AAGGC-TGCGGTGGACCGCTCCTGACTCCTGATGCTTCCCTTAGTCCCCTCCTCCCCTCC 3220
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                                                                                                                                                                                        2982 GACGGCCCTGAGTGCTGACCGCGTGAACAATATGAACATCAACGAGGGCAGCATAACGTT 3041
3010 GACAGCCCTCAGCGCTGACCGAGTGAACAATATCAACATCAACCAGGGCAGCATAACGTT 3041
3010 GACAGCCCTCAGCGCTGACCGAGTGAACAACATCAACATCAACCAGGGCAGCATCACGTT 3069
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                                       AAGGCGCCAGCGGACCCCTCCCGCCTCCCAGTGCTTCGCTCA-TCCCCTCCCTCCCTTCC
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                                                                                         CACCAAGGCCAAGAACGGGCACCTGGCTGTGGTGGCCCCCGCCGGCTGAACTCGCGGTGATG
                                                                                                      CACCAAGGCTAAGAATGGCCACCTGGCTGTGGTGGCCCCACGGCTGAATTCTCGGTGATG 3161
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (26-MAY-1993) Reizes O., UT-Southwestern Medical Center, Pharmacology, 5323 Harry Hines Boulevard, Dallas, Texas, USA, 7520 On Sep 3, 1993 this sequence version replaced gl:311501.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

1 (bases 1 to 3148)

Reizes,0., Barylko,B., Li,C., Sudhof,T.C. and Albanesi,J.P.

Domain structure of a mammalian myosin I beta

O/10/1970
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Bos taurus
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KFRGIISILDEECLRGGEFTDLYLFIEKLEDTIKGHPHITHKLADQRYRKSLDRGEFR
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TOFKMSILEIVFILKSRDAENDSUFFNKLADGFFDRSELSDKKRPETYA
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TOFKNSLLELVEILKSKEPAYVRCIKPNDSKOPGRFDEVLIRHQVKYLGLMENLRVRR
                                                                                                                                                                                                                                                                                                                   Dixon
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                                                            TACCTGGTGAAGGGCCAGTGTGCCAAGGTCTCCTCCATCAACGACAAGAGTGACTGGAAG 823
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                                                                                                                                                                                                           CGGGTGGTGCACCAAAATCACGGAGAGCGGAACTTCCACGTCTTTTACCAGCTACTGGAG 703
                                                                                                                                                                                                                                                                             TTTGACTTCAAGGGTGCCCCCGTGGGAGGCCACATTCTCAGTTACCTCCTGGAAAAGTCC
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                                                                                                                                                                                                                                                                                                                                                                             CGGGGTGGTGCTGCGGGACCGGCTGCTGCAGAGCAACCCGGTGCTGGAGGCCTTTGGC 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     AACCTCCGGCGGCGGTTCCGGGAGAACCTCATTTATACCTACATCGGTCCTGTCCTAGTC 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTGGGGGTACAGGACTTCGTGCTACTGGAGAACTTCACCAGCGAGGCCGCCTTCATCGAG 120
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               GTTATGAGGAAGGCGCTGTCCGTCATTGACTTCACTGAGGATGAAGTGGAGGACTTGCTC 883
                                                                                                                                                                                            CGGGTGCTGCACCAGAATCACGGGGAGAGGAACTTCCACATCTTCTACCAGCTGCTGGAG
                                                                                                                                                                                                                                                          TTTGACTTCAAGGGTGCCCCCGTGGGTGGCCACATCCTCAGTTACCTCCTGGAGAAGTCC
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RFPKTILFATEDALEIRRQSLATKIQATWRAFHCRQKFLRLKRSAICIQSWWRGTLGRR
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AGCATCGTGGCCAGCGTCCTACATCTGGGCAACATCCACTTTGCTGCTGACGAGGACAGC

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Qy	Db	Qy	Оу	Db Qy	Db 2	Q V	Qy	Db	₽ ₽	Qy	Db	Qy	Db	Db	Qy	Db	Qy	Qу	DЬ	Qy	Db	Qy	DЬ	QУ	DЪ	Qy	DP GA	Db
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CGCAAATATGAGGCTTTCCTGCAGAGGTACAAGTCACTGTGCCCAGAGACATGGCCCATG 20	TGAAGTACCTAGGGCTGATGGAGAACCTGCGTGTGCGCAGAGCCGGCTTTGCCTACC	AAAGTACCTGGGACTGATGGAGAATCTGCGCGTGCGCAGAGCT	ATCAAGCCAAACGACGCCAAGCAGCCGGGTCGCTTTGATGAGGTGCTCATCCGACATCAG 19	ATGAGCCTCCTGCAGCTCGTGGAGATCCTGAGGTCTAAGGAGCCTGCCT		TTGACAAGAGTGAGCTCAGTGACAAGAAGCGGCCAG-GACGGTGGCCACCCAGTTCAAG 1	CTCTTCCGGAACCTGAAGGAGACCATGTGCAGCTCAATGAACCCCATCATGGCCCAGTGC 1.		ATTATECTEGACGAGACGACCAGCGACCAGGAAATCTCTGGACCGCGGGGAGTTCCGCCTCCTG 1	TCGCTGACCAGAAGACCAGGAAATCCCTAGACCGAGGGGAGTTCCGCCTTCTG 1	TGACCTTCCTGGAGAAGCTGGAGGACACAATCAAGCAGCATCCACACTTCCTGACG	ACCTGACCTTTCTGGAGAAGTTGGAGGACACTGTCAAGCCCCACCCTCACTTCCTGACG 1	AAGTTCAAGGGCATCATCTCCATCTTGGATGAAGAGTGCCTGCGTCCTGGGGAGGCCACG 1.	GCGTGGGAACCGGTCCAGTATTTCAACAACAAGATTATCTGTGACCTGGTGGAGGAG	TCGCGTGGGAACCTGTCCAGTACTTCAACAACAAGATCATCTGTGACCTGGTAGAGGAG 1		AGCAGCTCTTCATCGAGCTGACTCTCAAGTCGGAGGAGGAGGAATACGAGGCTGAGGGC 1	GAAGTGTTTCAGCATAACAGCTTCGAGCAGTTCTGCATCAACTACTGCAATGAGAAGCTG 1: 		CTGAGAGCCCCAGCTGGCGAAGCACCACGGTTCTTGGGCTCCTGGACATTTACGGCTTT 1		ACAGCCGGACATTCACCTGGCTGGTCAGAAAGATCAATAGGTCACTGGCCTCTAAGGAC 1	CCCGCTGAACCTAGAACAGGCTGCATATGCACGGGACGCCCTCGCCAAGGCTGTG 1	TGAGCCCACTGAACCTTGAACAGGCGGCATATGCAAGGGATGCGCTTGCCAAGGCTGTG 1	TGCGGGAAGCCTGACCAACAGGAAGATCATCGCCAAAGGGGAAGAGCTC 1	GTACAACACTTAGGGAAGCCCTGACCCACAGGAAGATCATCGCCAAGGGGGAAGAGCTC 1	AATGCCCAGGTTACTACTGAGAACCAGCTCAAATATCTGACCAGGCTCCTTGGTGTGGAA AATGCCCAGGTCACTACTACTGAGAAAACCAGCTCAAATATCTGACCAGGCTCCTTGGTGTGTGAAA AACGCCCCAGGTCACCACGAGAACCAGCTCAAGTACCTGACCAGGCTCCTTGGTGTGGAA 9	
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3001 GCAGGGGGGGCGGGGGGGGGATGGCATTGACTTGACACCCGGGCTCGGAGCTGGTCATC 3060
                                                                   3043 GGAGGGGGTCCAGGCAGGGACGGCATCATTGACTTCACATCGGGCTCAGAGCTTCTCATC 3102
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                                                                                                                                                                                                       2021 GGAATCTCCGTCAGCAGCCTGAGCGACAGCCTCTTTGTGCTCCACGTGCAGGCGTGAGGAC 2880
                                                                                                                                                                                                                      2863 GGAATCTCTGTCAGTAGCCTGAGTGATAGCCTATTTGTGCTTCACGTGCAGCGTGAAGAC 2922
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                                                                                                                                                                                                                                                                                                                           2743 GTAAAATACGACGGTAAGGGGTTACAAGCCTCGCCCCGGCAGCTGCTGCTCACGCCCAGT 2802
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                                                                                                     2383 GCCTTCTTCTTGGACCACGTGCGCGCCCTCATTTTTGCTTAACCTGAGGCGCCAACTGCCC 2442
2341 GCCTTCTTCGTGGACCATGTGCGCACCTCTTTTCTGCTCAACCTTCGACGGCAGCTGCCC 2442
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2281 ACCATCCGGCGGCTCATCCAGGGCTTCATCCTGCGCCATGCGCCCGGTGCCCTGAGAAT 2382
2282 ACCATCCGGCGGCTCATCCAGGGCTTCATCCTGCGCCATGCGCCCGTTGCCCCTGAGAAT 2340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2083 GAAGAGTACAAAATGGGCAGGACTAAGATCTTCATCCGATTCCCCAAGACCTTATTTGCC 2142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2041 GAAGAGTACAAGATGGGCAGGACCAAGATCTTCATCCGCCTACCCCAAGACCCTGTTTGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1981 TGACAGGACGTCCCCAAGGATGGGGTGACTGTTCTGGTCAGGCACCTGGGCTACAAGCCG 2040
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42 CGGCCCTGGGCAGTGACGGGGTTCGAGTGACCATGGAGAGGGCCCTTGACTGCCCGAGACC 101
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Query Match Best Local Si Matches 2437;	BASE COUNT	CDS	TITLE JOURNAL MEDLINE PUBMED FEATURES SOURCE	REFERENCE AUTHORS TITLE JOURNAL REFERENCE AUTHORS	MAMIB LOCUS LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	ОУ 3 ДОУ 3 ДОУ 3
atch  2al Similarity 66.0%; Score 2417.6; DB 10; Length 2568; 2437; Conservative 0; Mismatches 14; Indels 1; Gaps 1.	/protuce-"myosin-I beta" /protuce-"myosin-I beta" /protuce-"myosin-I beta" /protuce-"caha7956.1" /db_xref="Caha67956.1" /db_xref="Gah67956.1" /db_xref="Mob:Mol:106612" /db_xref="Mob:Mol:106612" /db_xref="Mob:Mol:106612" /cranslation="MesslitanDargyQDEVLENETSEAAFIENLRGGFRENLITY ISGESGAGKTEATKRILGTYAETCPAPERGAVRORILGSNPYLEAPGMAKTLRNNS ILGANIHFANDESMACYTEROLKYLEKSDWKYMEALSRIPHVEYGLEGGEETLR RIGLERNPGSYLKLYKGQCAKVSSINUKSDWKYMEALSRIPHVEYGLEGEETLR RIGLERNPGSYLKLYKGQCAKVSSINUKSDWKYMEALSRIPHVEYGLESPL RIGLERNPGSYLKYKGCAKVSSINUKSDWKYMEALSRIPHVEYGLESPL RIGLERNPGSYLKYKGCAKVSSINUKSDWKYMEALSRIPHVEYGLESPL RIGLESPL RIGHTHANDESMACYTEROLKYLTRILGVEGTTLREALTHRKIAGEEDETLR NLEQAA7ARDALAKAVSFRTTYMLJKRINSLASKDAESPSWRSTTYLGLLSPL KFKGIISILDEECLREGEATDLTFLEKLEDTWKPHFLTHKLADKTYGFEV FOHNSEDGECINYCREKLOOLFIELTLKSDEEFYARSTYLGLUTYGFEV FOHNSEDGECINYCREKLOOLFIELTLKSDEEFYARSTYLGLUTYGFEV FOHNSEDGETADKINULLERNLETMCSSMNPHAQCEDKSELSDKKRPETVR RAGKRSLAGVTSYTGFLDKNUKLETMCSSMNPHAQCEDKSELSDKKRPETVR REPKTLEATELDRYKSLGPTWPMMAGREDGKNALTRHLGYKPEETKAERTKET REPKTLEATEDSLEFFRRSLATKIQAMRGEHMROKELKRHEGKLEVER RAAKRKMAQTIRRLIRGFILRHSPRCPENAFFLDHVRASFLLNLGRUPRNWGGTLGR FTPPPALID"  751 9 514 t		wattoi, M., Hamel, C., Fizenes, C., Levi-Acobas, F., Lenoir, M., Ripoll, C., Cloning of the genes encoding two murine and human cochlear graphols 40 (2), 332-341 (1997)  Location/Qualiflers  1 2556/Qualiflers	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; 1 (bases 1 to 2568) Crozet, F.  Direct Submission Submitted (30-JUL-1996) F. Crozet, Inst. Pasteur, Unite de ROUX, F. 75724, PARIS, Cedex 15, FRANCE Crozet, F. Amraoui, A. F. D. Vezet, FRANCE	2	3103 ACCAAGGCTAAGAATGGCCACCTGGCTGTGGTGGCCCCACGGCTGAATTCTCGGTGATGA 3162 3061 ACCAAGGCCAAGAACGGCCACCTGGCTGTGTGTGGTGGCCCCACGGCTGAATTCTCGGTGATGA 3162 3163 AGGC-TGCGGTGGACCGCTCCTGACTCC 3189 3121 AGGCCCAGCCGACCCCCCCCCCCCCCCCCCCCCCCCCC

<u> </u>	Qy 2141 Q 1121 Db 2215 C	1061 Qy 2081 Q	1001   Qy 2021 T 1074   Db 2095 T	TCAGCATCGTGGCCAGCGTCCTACATCTGGGCAACATCCACTTTGCTGCTGACGAGGACA         941         Qy         1961 GTC	AGGTTATGAGGAAGGCGCTGTCCGTCATTGACTTCACTGAGGATGAAGTGGAGGACTTGC 881	TGTACCTGGTGAAGGGCCAGTGTGCCAAGGTCTCCTCCATCAACGACAAGAGTGACTGGA 821	AGGGGGCGAGGAGACTCTCCGTCGGCCTGGGCTTGGAACGGAACCCCCAGAGCTACT       761       Qy       1781 AGA	CCCGGGTGGTGCACCAAAATCACGGAGAGCGGAACTTCCACGTCTTTTACCAGCTACTGG 701	1662 1735	1602 1675	1615	1555	1422 1495			AGAACCTCCGGGGGGGGGTTCCGGGAGAACCTCATTTATACCTACATCGGTCCTGTCCTAG 221	1255
JAGGGGCTTTCATTGGCGACAGAAATTTCTCCGGGTGAAGCGATCAGCCATCTGTATCC 	:CACAGAGGACTCCCTGGAAGTCCGGCGGCAGAGTCTAGCCACCAAGATCCAGGCGGCCT 	AGAAGAGTACAAAATGGGCAGGACTAAGATCTTCATCCGATTCCCCAAGACCTTATTTG 	GTGGGCAGGACGGCCCCAGGATGGTGTGGCCGTGTTGGTCAGACACCTCGGCTACAAGC 	PCGCAAATATGAGGCTTTCCTGCAGAGGTACAAGTCACTGTGCCCAGAGACATGGCCCA 	GOTGAAGTACCTGGGACTGATGGAGAATCTGCGCCTGCGCAGAGCTGGCTTTGCCTATC 	ONTCANGCCAAACGACGCCAAGCAGCCGGGTCGCTTTGATGAGGTGCTCATCCGACATC	ATGAGCCTCCTGCAGCTCGTGGAGATCCTGAGGTCTAAGGAGCCTGCCT	TTTGACAAGAGTGAGCTCAGTGACAAGAAGCGGCCAG-GACGGTGGCCACCCAGTTCA 	COTOTTCGGAACCTGAAGGAGACCATGTGCAGCTCAATGAACCCCATCATGGCCCAGT 	CATTATICCTGCAGAGGTGACCTACAGTGTGACTGGGTTTCTGGATAAAAAAATCACC 	S-ACAAGCTCGCTGACCAGAGACCAGGAAATCCCTAGACCGAGGGGAGTTCCGCCTTC 	SACCIGACCTTTCTGGAGAAGTTGGAGGACACTGTCAAGCCCCACCCTCACTTCCTGA 	AAGTTCAAGGCATCATCTCCATCTTGATGAAGAGTGCCTGCC	_ATCGCGTGGGAACCTGTCCAGTACTTCAACAACAAGATCATCTGTGACCTGGTAGAGG 	:CAGCAGCTCTFCATCGAGCTGACTCTCAAGTCGGAGCAGGAGGAATACGAGGCTGAGG 	(RAAGTGTTTCACCATAACAGCTTCGAGCAGTTCTGCATCAACTACTGCAATGAGAAGC 	SCTGAGAGCCCCAGCTIGGCGAAGCACCACGGTTCTTGGGCTCCTIGGACATTTACGGCT 

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
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Corey, D.P.
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Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea;
                                                                                                                  /TEASIALLION-"MESALTARDRYGODEFYLLENYTSEAAFIENLEKKEKENLTYTY
IGSVLVSVNPYKELELYSKOHMERYRGVSEYEVSPHYALADNSYRSLATERKDOCIL
ISGESGAGKTEASKKILQYYAVTGPYSDQVETYKORLLOSNPYLEAFGNAKTLRNDNS
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REGKYMDVOFDYKOAPVGGHILNYLLEKSRVYHONHGERNFHIFYOLLEGGEEDLLS
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VERNAKKHAVDVVRRETKGFIYRNOPROTENSFLJYNFORGAKTKHAYDFORS
VERAKHKONDLAFNNKYCRRINDEMROOLEOKVYKSLGKFREGVLLTONAKG
VERAKHKOOLESQTITTAVPVVKYDRAKGFRREDITLYRNOPROTENSFLJOKKSWPOS
VERAKHKOOLEOKTITTAVPVVKYDRAYRFRRROLLCITONANYL
TTARTILADELINTKILOOLESQTITTAVPVVKYDRAYRRRRRROLLCITONANYL
TTARTININTNINTNINGSTKEFFUNDERAGGEFTTATAVAVNOTISCHVORNYL
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                                                   /note="3 tandem IleGln motifs; encodes binding domains" 667 c 777 g 835 t
                                                                                               ITAEKINNININGGSIKFTYGPGKEGIIDFTAGSELLIAKAKNGHLSVVAPRLNSR"
2161. .2367
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mRNA, complete cds.
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Best Local Similarity 71.8%;
Matches 2270; Conservative
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                  TCAAATATCTGAGCAGGCTCCTTGGTGTGGGAAGGTACAACACTTAGGGAAGCCCTGACCC 1031
                                                          GAAATGTGCAGTTTGCCACAGATGAGCATGGACATGCCCAAGTCACAACAGAAAACCAGA 965
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                                                                                                                         ACTTCAATGATGATGATATAGAGGAATTGCTGAGCATTGTTGCTAGTGTACTACATTTGG
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0; Mismatches 891;
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JOURNAL REFERENCE AUTHORS TITLE

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2050 2045	91 ACAAGTCACTGTGCCCAGAGACATGGCCCATGTGGGCAGGACGGCCCCAGGATGGTGTGGGIIIIIIIIII	Oy 19 Db 19
1990 1985	31 TGCGCGTGCGCAGAGCTGGCTTTGCCTATCGTCGCAAATATGAGGCTTTCCTGCAGAGGT	Oy 19 Db 19
1930 1925	71 GTCGCTTTGATGAGGTGCTCATCCGACATCAGGTGAAGTACCTGGGACTGATGGAGAATC	Oy 18
1870 1865	11 TGAGGTCTAAGGAGCCTGCCTATATCCGGTGCATCAAGCCAAACGACGCCCAAGCAGCCGG	Оу 18 рь 18
1810 1805	52 AGCGGCCAG-GACGGTGGCCACCCAGTTCAAGATGAGCCTCCTGCAGCTCGTGGAGATCC	Qy 17 Db 17
1751 1745	92 GCAGCTCAATGAACCCCATCATGGCCCAGTGCTTGACAAGAGTGAGT	
1691 1685	32 TGACTGGGTTTCTGGATAAAAACAATGACCTCCTCTTCCGGAACCTGAAGGAGACCATGT	Qy 16 Db 16
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1451 1445	92 ACAACAAGATCATCTGTGACCTGGTAGAGGGAGAAGTTCAAGGGCATCATCTCCATCTTGG	Qy 13 Db 13
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1271 1265	12 CGGTTCTTGGGCTCCTGGACATTTACGGCTTTGAAGTGTTTCAGCATAACAGCTTCGAGC	Oy 12 Db 12
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1091 1085	32 ACAGGAAGATCATCGCCAAGGGGGGAAGAGCTCCTGGAGCCCACTGAACCTTGAACAGGCGGGIII	Oy 10

3131 TGGTGGCCCCACGGCTGAATTCTCGGTGATGAAGGCTGCGGT 3172 	Qy Db
3071 TTGACTTCACATCGGGCTCAGAGCTTCTCATCACCAAGGCTAAGAATGGCCACCTGGCTG 3130	Оу
3011 ATATCAACATCAACCAGGGCAGCATAACGTTTGCAGGGGGGTCCAGGCAGG	Оу
2951 AGAGTGATCATGTGATCGAGACACTAACCAAGACGGCCCTCAGTGCTGACCGCGTGAACA 3010	ОУ
2891 GCCTATTTGTGCTTCACGTGCAGCGTGAAGACAAGCAGAAGGGAGATGTGGTGCTGC 2950	Qу
2831 TCAAGCAGAGAATTGATTATGCCAACCTAACCGGAATCTCTGTCAGTAGCCTGAGTGATA 2890	Qy Db
2771 CTCGCCCCGGCAGCTGCTCACGCCCAGTGCTGGTGGTCATTGTGGAGGATGCTAAAG 2830	Оу
2711 GCTCTGAACCCATCCAGTATGCCGTGCCCGTGGTAAAATACGACCGTAAGGGTTACAAGC 2770	Qy Db
2651 TCTTCATTAGCACACGGCTTGGCACAGAGGAGCACCCCAGAGTGCTTCAATCCTTGG 2710	Qу
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2471 CACCCCACCTGCCCTGAGAGAGGCCTCAGAACTGCTACGGGAACTGTGCATGAAGAACA 2530	Оу Оъ
2411 CATTTTTGCTTAACCTGAGGCGGCAACTGCCCCGGAATGTTCTGGACACCTCCTGGCCCA 2470	Qy Db
2351 TTTTGCGCCATTCACCCCGGTGCCCTGAGAATGCCTTCTTCTTGGACCACGTGCGCGCCT 2410	Db Qy
2291 GGAAGGCAGCCAAGAGGAAGTGGGCAGCCCAGACCATCCGTCGACCATCCGTGGCTTCA 2350 	Qy Db
2231 TCCGGGTGAAGCGATCAGCCATCTGTATCCAGTCATGGGGGGGG	Qy Db
2171 AGAGTCTAGCCACCAAGATCCAGGCGGCCTGGAGGGGGCTTTCATTGGCGACAGAAATTTC 2230	Qy Db
2111 TCTTCATCCGATTCCCCAAGACCTTATTTGCCACAGAGGACTCCCTGGAAGTCCGGCGGC 2170 	Qy Db

RESULT 10 RCU14549 DEFINITION

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Query Match
Best Local Similarity 70.(
Matches 2269; Conservative
                                                                                72 CCATGGAGAGCGCCTTGACTGCCCGAGACCGGGTAGGGGTGCAGGACTTTGTCCTGCTGG 131
                                                                                                                                              12 CCGGGTCGGGAGGATGGGCTACCGGGCATCGGCCATGGGCAGTGACGGGGTTCGAGTGA 71
                                                              CCATGGAGAGTGCCTTAACAGCCCGAGATCGGGTTGGTGTCCAGGACTTTGTCCTGCTGG
                                                                                                                          CCCGGTGGAGTCGCATAGTGGGCAGCGTTCAGGCTCCAGCAATCGACGGGATCCGAATAA 111
                                                                                                                                                                                                                                                                                            1056 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (08-SEP-1994) Anne B. Metcalf, Cell
Neuroscience, University of Texas, 5323 Harry
TX 75235, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 3452)
Metcalf, A.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Metcalf, A.B., Chelliah, Y. and Hudspeth, A.J.
Molecular cioning of a myosin I beta isozyme that may mediate adaptation by hair cells of the bullfrog's internal ear proc. Natl. Acad. Sci. U.S.A. 91 (25), I1821-I1825 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi,
Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rana
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                                                                                                                                                                                                                                                                    IGSVLVSVIPYK ELEITYS KOHMERYGVODFVLLENYTSEAAF IENLEKREKENLITYY
ISGESCAGKTEASKKILQYYANTCEPVSDQVETVKDRLLANDNSYRSLRTEKDDCIL
SREGKYMDVOFDYKGAPVGGHILNYLLEKSRYVHONHGERNEH IFYQLLEGGEEDLIR
RIGLDKNAQNYOYLTKGQCARVSSINDKNEWKVVRRALSI INFNDDDIEELLSIVASV
RLEDAAVARDALAKAIYGRTESHLVSLESTVLRESLIHKKILAKGEELNSPL
KHGHVOFATDEHGHAQVTTENQIKYLARLISVDSTVLRESLIHKKILAKGEELNSPL
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LLHYAGEWYSVAGFLDKNNDLLFRNLKEVMDDSGNPIAHQCENSELTDKKRETAA
REPKILSTATEDALSVAGTVERVLARBLTDKKRETAA
REPKILFATEDALSVRGISVAGTLORDER
AGEAYRKKEIFLORKKOLFRULKEVMDDSGNPIAHQCENSELTDKKRETAA
REPKILFATEDALSVRHISIATTLQARWRCYHOROKFLHMKISAVEJSWRGTIGRR
VERLFITMTLGNDELTKKILOQLESGTLANSYLVSGIGYK PERFYKHGTARR
KAAKKWADVVRRETKGFITANOPROTENSYFLOYI RYSTIMTILYRODRKSVLDKSW
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VEEAKKKORIDYANITGISVSSLSDNLFYLLHVKCEDNKOGTKEFKOKKDNYPOS
TAAKKINININNOGSIKFTVGPGREGIIDFTAGSELLIAAKKNGHLSVVAAPRLIKAA

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Rana cate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /Product="nyosin I beta"
/Protein_id="AAA57192.1"
/b_xcef="GI:602138"
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/note="partially processed transcript"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Join(114. 2029,2110. 3280)

'gene="AMI beta"

join(114. 2029,2110. 3280)

'gene="AMI beta"
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/db_xref="taxon:8400"
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join(114. .2029,2116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
1. .3452
                                                                                                                                                                                                                           44.68;
70.08;
                                                                                                                                                                                                     Score 1632.8;
Pred. No. 0;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                          892 ACTTCAATGATGATATAGAGGAATTGCTGAGCATTGTTGCTAGTGTACTACATTTGG
                                                                                                                                                                                                                                                                                                                                                                                                    832 TTAGCTCAATCAATGATAAAAATGACTGGAAGGTTGTTAGGCGAGCCTTGTCAATTATAA 891
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            712 GAAACTTCCATATTTTTTACCAGCTTCTTGAGGGTGGAGAAGAGGATTTGCTACGGAGGC
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                                                             GAAAGATCAATAGGTCACTGGCCTCTAAGGACGCTGAGAGCCCCAGCTGGCGAAGCACCA 1211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    592 CCAGCCCCTTCGGAAAATATATGGATGTGCAATTTGATTACAAGGGAGCTCCTGTCGGTG
                                                                                                           CTTATGOTCGAGATGCCTTGGCCAAAGCAATCTATGGCCGTACCTTCTCCTGGCTTGTTA 1191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                492 TGCAGAGCAACCCCGTGTTAGAGGCCTTTGGGAATGCCCAAGACTCTCCGCAACGATAACT
                                                                                                                                                       ACAAAAAGATTATTGCTAAAGGAGAAGAGCTGAACAGTCCACTTAACCTGGAGCAAGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    552
                                                                                                                                                                                                                   TTAAATACCTCGCCAGGCTCCTCTGTAGACTCTACTGTACTACGGGAGTCTCTCATTC
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                                                                                                                                                                                                                                    TCAAATATCTGAGCAGGCTCCTTGGTGTGGGGAAGGTACAACACTTAGGGAAGCCCTGACCC 1031
                                                                                                                                                                                                                                                                           GAAATGTGCAGTTTGCCACAGATGAGCATGGACATGCCCAAGTCACAACAGAAAACCAGA 1011
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                                                                                                                                                                                                                                                                                                                                                           ACTTCACTGAGGATGAAGTGGAGGAGCTTGCTCAGCATCGTGGCCAGCGTCCTACATCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   312 ATTTGTTTGCAGTGGCTGACACTGTATACCGGGCACTTCGTACTGAGCGTCGGGACCAGG 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTCCTCCATCAACGACAAGAGTGACTGGAAGGTTATGAGGAAGGCGCTGTCCGTCATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGGGCTGGATAAAAATGCCCAAAATTACCAGTACTTGATTAAGGGTCAGTGTGCCAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCAGCCGGTTTGGAAAGTACATGGATGTGGAGTTTGACTTCAAGGGTGCCCCGTGGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGCAGTCCAATCCTGTTTTGGAGGCATTTGGCAATGCAAAAACCTTACGAAATGATAATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGTACTATGCTGTGACGTGTCCTGTCAGTGACCAGGTGGAGACTGTGAAAGACCGACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATATATATGCCATAGCAGATAACTCCTACCGCTCCTTGCGCACAGAGAGAAGAACAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCTACAGCCGGCAGCATATGGAACGCTACCGTGGTGTCAGTTTCTATGAAGTACCACCTC 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCATATATACGTACATTGGGTCAGTCTTGGTATCTGTCAATCCTTACAAAGAGTTAGAGA 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGAATITCACCAGTGAGGCTGCCTTCAITGAGAACCTCCGGCGGCGGTTCCGGGAGAACC
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FEATURES

CDS gene JOURNAL

JOURNAL MEDLINE PUBMED REFERENCE AUTHORS TITLE

AUTHORS

TITLE

SOURCE ORGANISM ACCESSION VERSION KEYWORDS

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BASE COUNT ORIGIN

951

831

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611 591 551 531

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2270	TCATTGGCGACAGAAATTTCTCCGGGTGAAGCGATCAGCCATCTGTATCCAGTCATGGTG	2211	Qy
2210 2331	CTCCCTGGAAGTCCGGCGCAGAGTCTAGCCACCAAGATCCAGGGGGCCTGGAAGGGGCTT	2151 2272	Оу
2150 2271	CAAAATGGGCAGACTAAGATCTTCATCCGATTCCCCAAGACCTTATTTGCCACAGAGGA	2091 2212	Db Oy
2090 2211	ACGGCCCCAGGATGGTGTGGCCGTGTTGGTCAGACACCTCGGCTACAAGCCAGAAGAGTA	2031 2152	ОУ
2151	ANTATTGTGGTTTCCTAGGTACAAATCTCTTTGCCCTGATACTTGGCCTAACTGGGATGG	2092	DB 4
9	TGAGAACAAGTGAAATGTTGTGTATGGAAGGCACTTGCCCCCACATTATTATGCATGTATT	0	B B
1985		1986	Qy
1985 2031	TGCGCGTGCGCAGAGCTGGCTTTGCCTATCGTCGCAAATATGAGGCTTTCCTGCA	1931	Db Qy
97		91	рb
1930	GTCGCTTTGATGAGGTGCTCATCCGACATCAGGTGAAGTACCTGGGGACTGATGGAGAATC	1871	Q
1870 1911	TGAGGTCTAAGGAGCCTGCCTATATCCGGTGCATCAAGCCAAACGACGCCCAAGCAGCCGG 	1811 1852	DB Qy
1810 1851	AGCGGCCAG-GACGGTGGCCACCCAGTTCAAGATGAGCCTCCTGCAGCTCGTGGAGATCC	1752 1792	Оy
1751 1791	GCAGCTCAATGAACCCCATCATGGCCCAGTGCTTTGACAAGAGTGAGCTCAGTGACAAGA	1692 1732	Ф
1691 1731	"IGACTGGGTTYCTGGATAAAAKCAATGACCTCCTCTTCCGGAACCTGAAGGAGACCATGT 	1672	д . У
0 0	ATTCCTAGACCGAGGGAGTTCCGCCTTCTGCATTATGCTGGAGAGGTGACCTACAGTG	61	D 04
1571 1611	ACACTGTCAAGCCCCACCCTCACTTCCTGACGCACAAGCTCGCTGACCAGAAGACCAGGA	1512 1552	Db Qy
1511 1551	ATGAAGAGTGCCTGCGTCCTGGGGAGGCCACGGACCTGACCTTTCTGGAGAAGTTGGAGG	1452 1492	Db Qy
1451 1491	ACAACAAGATCATCTGTGACCTGGTAGAGGAGAAGTTCAAGGGCATCATCTCCATCTTGG	1392 1432	Db
1391 1431	AGTCGGAGCAGGAGGAATACGAGGCTGAGGGCATCGCGTGGGAACCTGTCCAGTACTTCA	1332 1372	Оy
1331 1371	AGTTCTGCATCAACTACTGCAATGAGAAGCTGCAGCAGCTCTCATCATCGAGCTGACTCTCA	1272 1312	Qу
1311		1252	Db

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RESU AYO6 LOCU DEFI ACCE VERS	ОУ	DЪ	Qy	Db,	рь	рь	8	5 6	Db Qq	g B	Qy	Db	Qy	Qу Дъ	дь Q2	Вb	γQ	Db XX	2 (	Db Db	Ъ	QY	₽ 2	Qy	ф
LT 11 9044 S NITIO SSION ION	3171 3292	232	3111	3051 3172	3112	05	93	2871	2932	87	2751	81	2691	2631 2752	2692	632	511	57	7 1	2391 2512	2452	2331	39	27	2332
AY069044 AY069044 3445 bp mRNA linear INV 17- N Drosophila melanogaster GH04201 full length cDNA. AY069044 AY069044 GI:17861423	GT 3172 	ACACTTGTGTGTTGCTCCTCGTCTGAATTCACGATGATGACCACTG	TAAGAATGGCCACCTGGCTGTGGTGGCCCCACGGCTGAATTCTCGGTGATGAAGGCTGCG	TCCAGGCAGGGACGGCATCATTGACTTCACATCGGGCTCAGAGCTTCTCATCACCAAGGC	CASTSCTSACCSSTSAACAATATCAACATCAACCASSCASCATACCSTTSCASSSSS		AAGGGAGATGTGGTGCTGCAGAGTGATCATGTGATCGAGACACTAACCAAGACGGCC	TGTCAGTAGCCTGAGTGATAGCCTATTTGTGCTTCACGTGCAGCGTGAAGAACAACAACAACAACAACAACAACAACAACAACAAC	CATTGTGGAGGATGCTAAAGTCAAGCKGAGATTGATTATGCCAACCTAACCGGAATCTC	GACAGAAAGGGGTACAAGCCCCGGAGAAGACAACTTCTGCTCACTCA	CGACCGTAAGGGTTACAAGCCTCGCCCCCGGCAGCTGCTGCTCACGCCCAGTGCTGGT		AGTGCTTCAATCCTTGGGCTCTGAACCCATCCAGTATGCCGTGCCCGTGGTAAAATA	CCCCCAGAGTGTCCCCAGACTCTTCATTAGCACACGGCTTGGCACAGAGGAGATCAGCCC	GCAGCAGCTGCAGCAAAAGGCGGTGGTAGTGAAATTTTCAAGGGCAAGAAGGACAACTA		rgcatgaagaacatggtgtggaagtactgccggagcatcagccctgagtggaa	TCCTGGCCTGTGCCACCTCCATCGCTCAGAGAGAGGCCTCTGAGCTCCTGAG	TO A CONTROLL OF THE CONTROLL	CTTGGACCACGTGCGCGCCTCATTTTTGCTTAACCTGAGGCGGCAACTGCCCCGGAATGT	TTTTATCAAAGGCTTCATTTACCGCAATCAACCCCGTTGCACTGAGAATGAGTACTT	GACTCATCCGTGGCTTCATTTTGCGCCATTCACCCCGGTGCCCTGAGAATGCCTTCTT		GTGGCACACTGGGCCGGAGGAAGGCAGCCAAGAGGAAGTGGGCAGCCCAGACCATCCG	TCATCAACGACAGAAATTCCTGCACATGAAACATTCCGCGGTAGAGATCCAGTCGTGGTG
DEC-200		3291	3170	3110 3231	3171	11	99	2930	2991	93	2810	87	2750	2690 2811	2751	69	2570	63	л ,	2450 2571	2511	2390	45	ω ω	2391

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                                     907
                                                   PETALIPOTES AND LEFT LANGUAGE THE THE LANGUAGE THE THE LANGUAGE THE LANGUAGE THE THE LANGUAGE THE THE LANGUAGE THE THE LANGUAGE THE THE
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Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory

Elerkeley, CA 94720
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Drosophila melanogaster
Eukaryota; metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila;
1 (bases 1 to 3445)
1 (bases) Trosophila; Arthropoda; Arthrop
                                ದ
                                {	t PRIIEFSTYIIDTVGTASIVSIVDRNSLEHNVVKGKGGVIDIQTGAEPGVVRDKGHLV}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product-"GH04201p"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="Myo61F"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ...Oce "alignment with genomic scaffold AE003471"
/db_xref="FLYBASE:FBgn0010246"
117. .3224
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/map="61F6-61F7"
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FEATURES

CDS

0; Length 3445; 6

46 CCTGGGCAGTGACGGGGTTCGAGTGACCATGGAGAGGGCCTTGACTGGCCGAGACGGGT Conservative 25.1%; 58.6%; Score 919.6; DB 3; Pred. No. 1.1e-220; 0; Mismatches 1189; Indels

COMMENT

TITLE JOURNAL

REFERENCE AUTHORS

KEYWORDS SOURCE

166 CCTCCGGCGGCGCTTCCGGGAGAACCTCATTATACCTACATCGGTCCTGTCCTAGTCTC TCTGAAGAAGCGGTTCCAGGAGGACCTGATCTATACCTACATTGGCCAGGTGTTGATCTC 295

286 TGTCAGTTTCTATGAAGTACCACCTCATTTGTTTGCAGTGGGCTGACACTGTATACCGGGC 296 COTGAATCCCTACAAGCAGCTGCCCATCTACACCGATGACCATGTCAAGGCGTACAGAAA TGTCAATCCCTACCGAGACCTACAGATCTACAGCCGGCAGCATATGGAACGCTACCGTGG 285 355

406 GACAGAGGCCAGCAAGAGAGTGCTCCAGTTCTATGCAGAGACCCTGCCCAGCCCCTGAACG 465 416 GOTGATCGAGGAGAACCGCGGCCAGTGCGTGCTCATCTCCGGGAGAGAGTGGTTCCCGGCAA GACAGAGGCCTCCAAGAAGGTGCTGCAGTTCATAGCCGGCTGCTCCGGGCAACCAGACGAC

536 CÓTCGAGGGCGTCAAGGACAAGCTGCTAAAGAGCAATCCCGTGCTGGAGGCCTTCGGCAA 466 GGGTGGGGCAGTGCGAGACCCCCCTTTTGGGAGCCAACCCCCGTGTTAGAGGCCTTTTGGGAA 525

TGCCAAGACTCTCCGCAACGATAACTCCAGCCGGTTTGGAAAGTACATGGATGTGCAGTT 585 TGCCAAGACAAACGGCAATGACAACTCCTCGCGGTTCGGCAAGTACATGGACATCCAGTT

656 CGATTTCAAAGGAGCTCCGATCGGAGGCAACATCCTAAACTATCTGCTGGAAAAGTCGCG TGACTTCAAGGGTGCCCCCCGTGGGAGGCCACATTCTCAGTTACCTCCTGGAAAAGTCCCG

716 AGTGGTGGCTCAAATGGGAAGGGGGAACGTTCCACATCTTCTACCAACTCTTGGCCGG GGTGGTGCACCAAAATCACGGAGAGCGGAACTTCCACGTCTTTTACCAGCTACTGGAGGG

705

645 655

776 GGCGACGAGGCCCTTCTGCAGGAACTGCGCCTGGAGCGGGCTCTGGACACTTATAGCTA 706 GGGCGAGGAGGACTCTCCGTCGGCTGGGCTTGGAACGGAACCCCCAGAGCTACTTGTA 765

CCTGACAGATGGGCTCAATGGCACCGTGACGAGAATTAACGATGCGGACAGCTTCAAGCA 895 CCTGGTGAAGGGCCAGTGTGCCAAGGTCTCCATCAACGACAAGAGTGACTGGAAGGT 825

826 TATGAGGAAGGCGCTGTCCGTCATTGACTTCACTGAGGATGAAGTGGAGGACTTGCTCAG 885 GGTCCAGCAGGCTCTCACTGTGATCGATTTCACCAAGGAGGAGCAGCAGCGCGAGATCTTCGG

TGCCAAGGTGAACAGCAGGGATCTGGTAGTCACCGCTGCTCGTTTGCTGGGTGTAAACGC TGCCCAGGTTACTACTGAGAACCAGCTCAAATATCTGACCAGGCTCCTTGGTGTGGAAGG 1005

BASE COUNT

1073 AAGCGAACTGGAAGCCGCCTAACGCACCGCACAATTGACGCTCGGGGAGATGTGGTGAC 1132 TACAACACTTAGGGAAGCCCTGACCCACAGGAAGATCATCGCCAAGGGGGAAGAGCTCCT 1065

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ACCESSION VERSION KEYWORDS

007596.1

GI:466257

Drosophila melanogaster U07596

3382 bp myosin-IB

mRNA, mRNA

complete linear

cds.

INV 08-JUL-1994

DMU07596

SOURCE

ORGANISM

fruit fly.

Drosophila melanogaster

Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;

Neoptera; Endopterygota; Diptera; Brachycera; Muscc

Ephydroidea; Drosophilldae; Drosophila.

ecta; Pterygota;
Muscomorpha;

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RESULT 12
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                                                                                  199 GAGGACCTGATTTATACCTACATTGGCCAGGTGTTGATCTCCGTGAATCCCTACAAGCAG 258
                                                                                                                    185 GAGAACCTCATTTATACCTACATCGGTCCTGTCCTAGTCTCTGTCAATCCCTACCGAGAC 244
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Direct Submission
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//note-*amino acids 1-693, typical myosin head domain; amino acids 694-765, neck domain containing 3 IQ motifs; amino acids 766-1026, unique tail domain"
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McKenna"
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                                                                        CGACAGAAATTTCTCCGGGTGAAGCGATCAGCCATCTGTATCCAGTCATGGTGGCGTGGC
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                      CACGTGCGCGCCTCATTTTTGCTTAACCTGAGGCGGCAACTGCCCCGGAATGTTCTGGAC
                                                                                                                                                                                                                                                                                                          CAGGAGAAGAAACATGAGATAGCGGCCATCATCCAGGCCCACTGGAAGGGATTGATGCAG
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AACGCCAAGCGTATGTGGCTGCTTCGACTGGCGAAGGAGCTGCCCACCAAGGTGCTAGAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTCATTGTGGAGGATGCTAAAGTCAAGCAGAGAATTGATTATGC---CAACCTAACCGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GACTTCGTGGCCAGCACCTTCGGCAGCGAGCAGCTTAAGTACCAGTCCTTCTGCACCAAG
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Submitted (03-NOV-1999) Celera Genomics,
Rockville, MD, USA
This sequence was identified as CDM:10210
                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 116374)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HTG; HTGS_PHASE2.
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                                                                                                                                                                                                                                                                                                                                                        Adams, M. and Venter, J.C
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                                                                                                                                                                                                                                                   fly@celera.com
                                                                                                                                                                           This sequence will be replaced
by the finished sequence as soon as it
the accession number will be preserved
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                                                                                     /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
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CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	CTGTCAAGCCCAGCACCACACACACACACACACACAACAGATCAGCAACACACAACAACAACACACAC
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1575 CCCTRAGACGAGGGGAGTTCCCGCCTTCTGATTATGCTGCAGCACATCAÁGÁÁA 5489 TCATGCTGCGCGATAAATCAGCTCCTTCTGCATTATGCTGCAGGGGAGGGA	CGGAGCAGGATGAAGACCACCACCACCACGAGGAGGGCACCAGGAGGACCACGACACCAC
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CCCACA TGACCT ICACCT IC	GGAG
CACATCAC  CACATCAC  CACATCAC  CACACCAC  CACACCAC  CACACCAC  CACACCAC	TTG CTC.
AAGAAAAT : AACT 3 CC 2 2 CC 2 3 CC 2 C	ACCO
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	COURGEAGGCATCCAGAAAACCTCCAGAAAACCTCCAGAAGACACACAC
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JOURNAL REFERENCE
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AUTHORS
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                                                                                     AUTHORS
                                                                                                                                                                                                       TITLE
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                                                                                                                                                                                                                           Abams, M.D., Holt, R.A., Evans, C.A.,
Gocayne, J.D., Tabor, P., Williamson, A., Homsi, F.H.,
Dugan-Rocha, S.D., Sodergren, E.S., Hodgson, A.H., Chen, R.C.,
Ayele, M., Scott, G.S., Worley, K.W., Amamatides, P.G., Brandon, R.C.,
Rogers, Y., An, H., Baldwin, D., Beeson, K.Y., Brown, M., Buhay, C.,
Busam, D.A., Center, A., Chen, G., Chen, Z., Clerc-Blankenburg, K.,
Davenport, L.B., Dietz, S.M., Ding, Y., Dodson, K., Doup, L.E.,
Davenport, L., Emery-Cohen, A., Ferriera, S., Garg, N.D.S., Houck, J.,
Hostin, D., Howland, T.J., Hume, J., Ibegwam, C., Jalali, M., Kovar, C.,
Liu, W., Mattel, B., McIntosh, T.C., Morgan, M., Moy, M., Murphy, B.,
Nelson, K.A., Ndassa, Y., Nguyen, N., Perez, L., Pittman, G.S., Puri, V.,
Scheeler, F., Shen, H., Strong, R., Tector, C., Wang, Q., Williams, S.M.,
Wheeler, D., Weinstock, G., Gibbs, R. and Venter, J.C.
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 175481)
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                                    Worley,K.C., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J.
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AC010007.4 GI:21306589
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    Bimage, K.,
    Blankenburg, K.,
Bonnin, D., Bouck, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34230
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Davy Carroll L. Dederich, D.A., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Elagar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Elagar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagy, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lozado, R.J., Lu, X., Lucler, A., Lucler, R., Lucler, R., Luna, R., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Meis, G., Merzker, M., Menz, G., Miner, S., Mitchell, T., Mohabbat, K., Morgan, M., Morifs, S., Moser, M., Neal, D., Newtson, J., Newtson, N., Nguyen, N., Nickerson, E., Nwokenkwo, S., Oguh, M., Okwuonu, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L. L., Quiles, M., Ren, Y., Rives, M., Rejas, A., Rojubokan, I., Rolfe, M., Stanley, H., Stone, H., Shooshtari, N., Stone, H., Shooshtari, N., Stone, H., Shooshtari, N., Stone, H., Shooshtari, N., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Tamsey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Tamsey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Taylor, C., Williams, G., Williamson, A., Weczyk, R., Wooden, S., Weisen, P., Stone, R., Wooden, S., Weisen, R., W Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.F., Buhr Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F. Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., C. Unpublished 3 (bases 1 Direct Submission

REFERENCE AUTHORS

JOURNAL REFERENCE AUTHORS

TITLE

Worley, K.C.

(bases 1 to 175481)

Direct Submission

JOURNAL

TITLE

Submitted (11-SEP-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 175481)
Worley, K.C., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J.,

Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N. B., Bhowle, S., Brieva, M., Brown, E., Brown, M., Bryant, N. B., Burnaty, C., Burch, P., Bursett, C., Burcell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chargo, T.F., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Davy-Carroll, L., Dinh, H.H., Douthwaite, K.J., Draper, H., Denn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Denn, A.L., Ding, Y., Dinh, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elhaj, C., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Garra, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Harris, C., Hodgson, A., Hogues, M., Holloway, C., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hullyk, S., Hume, J., Jackson, L.E., Jacobson, B., Jia, Y., Johnson, R., Jollvet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lewis, L.C., Liu, J., Liu, W., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Lewis, L. C., Liu, J., Liu, M., Martin, R., Martindale, A., Mousen, N., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., Nguyen, N., Nickerson, E., Race, A., Payton, B., Oguh, M., Okwison, R., Olyiedo, R., Dace, A., Payton, B., Condan, M., Martindale, A., Davido, R., Oragunye, N., Oviedo, R., Pace, A., Payton, B.,

COMMENT

REFERENCE AUTHORS TITLE

JOURNAL

JOURNAL

Submission

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ANNOTATION OF FEATURES:

STSS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

(Nuc. Acids Res. 25:3389-3402) similarity are identified by BLAST flanked by consensus splice sites that maintained sequence continuity across the splice sites that maintained sequence identical matches are annotated as similar.
                                                                                                                                                                                                                                                                                                                                                                                                     OUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found to URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCING READ COVERAGE: Sequencing is completed to a minimum reads with a minimum of 2 clones and 2 clones and 3 reads with a minimum of 2 clones and 2 clones and 3 reads with no ambiguities or 2 chemistries with a minimum of 2 a region does not meet this standard, it will be indicated in the annotation as Low Coverage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones.

Overlapping clones are noted at the beginning and end of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (01-JUN-2002) Human Genome Sequencing Center, Deposit of Molecular and Human Genetics, Baylor College of Medicing Baylor Plaza, Houston, TX 77030, USA On Jun 1, 2002 this sequence version replaced gi:17998562.

IMFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quilles, M., Ren, Y., Rives, M., Rojas, A., Rojubokan, I., Rolfe, M., Rojas, A., Severy, G., Scherer, S., Scott, G., Shen, H., Shoshtari, N., Stone, H., Sutton, A., Syarke, T., Sparks, A., Stanley, H., Tang, H., Tansey, J., Taylor, T., Tabor, P., Tamerisa, A., Tamerisa, K., Wall, R., Wand, K., Vasquez, L., Vera, V., Villaion, D., Vinson, R., Watlington, S., Walliams, G., Warren, R., Washington, C., Wu, Y., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Nelson, D., Ninson, R., Weinstock, G. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (29-DEC-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Saylor Plaza, Houston, TX 77030, USA
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/function="polymorphic site"
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                                                             Db 107605 TCACCAAGGAGGAGCAGGGGGAGATCTTCGGAATCGTGGCCAGCATTCTGCATCTAGGAA 107664
                                                                                                                                                          δÃ
                                                                                                                                                                                                Db 107545
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                                                                                                                                                                                                                                                                                                                                                                                                            Db 107365 TTCCACATCTTCTACCAACTCTTGGCCGGCGCGCGACGAGGCCCCTTCTGCAGGAACTGCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 107245 CGGTTCGGCAAGTACATGGACATCCAGTTCGATTTCAAAGGAGCTCCGATCGGAGGCAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Db 107065 CTCATCTCCGGAGAGAGTGGTTCCGGCAAGACAGAGGCCTCCAAGAAGGAGGTGCTGCAGTTC 107124
                                                                                                                                                                                                                                   107485 GGGTATTGACAATTGGTCTCTGATCTTCGAGTTCTAATCCACAGCTCAATGGCACCGTGA 107544
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915 ACATCCACTTTGCTGCTGACGAGGACAGCAATGCCCAGGTTACTACTGAGAACCAGCTCA 974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107185 AGCAATCCCGTGCTGGAGGCCTTCGGCAATGCCAAGACAAACCGCAATGACAACTCCTCG 107244
                                                                                                                                                                             795 CCTCCATCAACGACCAAGAGTCACTGGAAGGTTATGAGGAAGGCGCTGTCCGTCATTGACT 854
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                         737 TTGGAACGGAACCCCCAGAGCTACTTGTACCTTGGTGAAGGGCCAGTGTGCCAAG------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          377 ATGATTTCTGGAGAGAGTGGGGGCAGGCAAGACAGAGACAGAGACTGCTCCAGTTC 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               317 TTTGCAGTGGCTGACACTGTATACCGGGCACTTCGTACTGAGCGTCGGGACCAGGCAGTG 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
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                                                                                                       TCACTGAGGATGAAGTGGAGGACTTGCTCAGCATCGTGGCCAGCGTCCTACATCTGGGCA 914
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATCCTAAACTATCTGCTGGAAAAGTCGCGAGTGGTGGCTCAAATGGGAAGGCGAAGCGAAC 107364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGGTTTGGAAAGTACATGGATGTGCAGTTTGACTTCAAGGGTGCCCCCGTGGGAGGCCAC 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGCAACCCCGTGTTAGAGGCCTTTGGGAATGCCAAGACTCTCCGCAACGATAACTCCAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TATGCAGAGACCTGCCCAGCCCCTGAACGGGGTGGCGCAGTGCGAGACCGCCTGTTGCAG 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTTGCGGTGACTGACAACGCCTTCCGTTCGCTGATCGAGGAGAACCGCGGCCAGTGCGTG 107064
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Calling a C and should /function="polymorphic site" 24987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Calling a C and /function="polymorphic
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24185
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/function="polymorphic site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20.5%; Score 749.4; DB 3; 57.1%; Pred. No. 1.3e-177;
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FEATURES

source

misc\_feature

/note-"Calling

/note="Calling a C and

function="polymorphic

/organism="Drosophila /db\_xref="taxon:7227" /chromosome="3L"

Location/Qualifiers

/clone="RP98-17K17"

misc\_feature misc\_feature

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1993 108732	GCGTGCGCAGAGCTGGCTTTGCCTATCGTCGCAAATATGAGGCTTTCCTGCAGAGGTACA	1934 108673	ОУ
1933 108672	GCTTTGATGAGGTGCTCATCCGACATCAGGTGAAGTACCTGGGACTGATGGAGAATCTGC	1874 108613	ОУ
1873 108612	GGTCTAAGGAGCCTGCCTATATCCGGTGCATCAAGCCAAAGGACGCCAAGCAGCCGGGTC	1814 108553	Qy Db
1813 108552	GGCCAG-GACGGTGGCCACCCAGTTCAAGATGAGCCTCCTGCAGCTCGTGGAGATCCTGA	1755 108493	Db Qy
1754 108492	GCTCAATGAACCCCATCATGGCCCAGTGCTTGACAAGAGTGAGCTCAGTGACAAGAAGC	1695 108433	90 V2
1694 108432	CTGGGTTTCTGGATAAAACAATGACCTCCTCTTCCGGAACCTGAAGGAGACCATGTGCA	1635 108373	P 64
1634 108372	CCCTAGACCGAGGGAGTTCCGCCTTCTGCATTATGCTGGAGAGGTGACCTACAGTGTGA	1575 108313	Qy db
1574 108312	CTGTCAAGCCCCACCCTCACTTCCTGACGCACAAGCTCGCTGACGAAGAAGACCAGGAAAT	1515 108253	D\$
1514 108252	AAGAGTGCCTGCGTCCTGGGGAGGCCACGGACCTGACCT	1455 108193	Qy db
1454 108192	ACAAGATCATCTGTGACCTGGTAGAGGAGAAGTTCAAGGGCATCATCTCCATCTTGGATG	1395 108133	Db
1394 108132	CGGAGCAGGAGGAATACGAGGCTGAGGGCATCGCGTGGGAACCTGTCCAGTACTTCAACA	1335 108073	D Q
1334 108072	TCTGCATCAACTACTGCAATGAGAAGCTGCAGCAGCTCTTCATCGAGCTGACTCTCAAGT	1275 108013	Фр
1274 108012	TTCTTGGGCTCCTGGACATTTACGGCTTTGAAGTGTTTCAGCATAACAGCTTCGAGCAGT	1215 107953	Оy
1214 107952	AGATCAATAGGTCACTGGCCTCTAAGGACGCTGAGAGCCCCAGGCTGGCGAAGCACCACGG	1155 107902	Db Qy
115 <b>4</b> 107901	ATGCAAGGGATGCGCTTGCCAAGGCTGTGTACAGCCGGACATTCACCTGGCTGG	1095 107842	Db dd
1094 107841	GGAAGATCATCGCCAAGGGGGAAGAGCTCCTGAGCCCACTGAACCTTGAACAGGCGGCAT	1035 107782	Db Qy
1034 107781	AATATCTGACCAGGCTCCTTGGTGTGGGAAGGTACAACACTTAGGGAAGCCCTGACCCACA	975 107722	Qy Db
107721	ACGTTGGCTTCACTGAGGTGGAGGGCAATGCCAAGGTGAACAGCAGGGATCTGGTAG	107665	В

ACCESSION

AC005847 268369 bp DNA linear INV 22-OCT-1998 Drosophila melanogaster DNA sequence (P1s DS03179 (D226), DS06357 (D230), DS03404 (D231), DS06962 (D232), and DS07291 (D240)), complete sequence.

AC005847 AC004331 AC004436 AC004334 AC004488 AC004489

RESULT AC0058 LOCUS DEFINIS	Qy Db:	Qy Db 1	Оу	Qy Db 1	Qy Db 1	Qy Db 1	Qy Db 1	Qy Db 1	Qy Db 1	Qy Db 1	Qy Db 1	Qy Db 1	Qy Db 1	Qy Db 1	Qy Db 1	Qy Db 1
RESULT 15 AC005847/c LOCUS DEFINITION	2936 109693	2876 109633	2819 109573	2759 109513	2699 109453	2648 109393	2588 109333	2528 109273	2468 109213	2408 109153	2348 109093	2288 109033	2228 108973	2168 108913	2108 108853	2048 108793
2 AC005847 268369 bp DNA linear INV 22-OCT-1998 V Drosophila melanogaster DNA sequence (P1s DS03179 (D226), DS06357 (D230), DS03404 (D231), DS06962 (D232), and DS07291 (D240)),	GAGATGTGGTGCAGAGTGATCATGTGATCGAG 2970 	GTAGCCTGAGTGATAGCCTATTTGTGCTTCACGTGCAGCGTGAAGAACAACAAGCAGAAGG 2935	AGGATGCTAAAGTCAAGCAGAGAATTGATTATGCCAACCTAACCGGAATCTCTGTCA 2875	AGGGTTACAAGCCTCGCCCCGGCAGCTGCTGCTCACGCCCAGTGCTGTGGTCATTGTGG 2818	TTCAATCCTTGGGCTCTGAACCCATCCAGTATGCCGTGCCGTGGTAAAATACGACCGTA 2758	GACTCTTCATTAGCACACGGCTTGGCACAGAGGAGATCAGCCCCAGAGTGC 2698	AGGCGGTGGCTAGTGAAATTTTCAAGGGCAAGAAGAAGAACTACCCCCAGAGTGTCCCCA 2647	ACATGGTGTGGAAGTACTGCCGGAGCATCAGCCCTGAGTGGAAGCAGCAGCTGCAGCAAA 2587	CCACACCCCCACCTGCCCTGAGAGAGGGCCTCAGAACTGCTACGGGAACTGTGCATGAAGA 2527	CCTCATTTTTGCTTAACCTGAGGGGGCAACTGCCCCGGAATGTTCTGGACACCTCCTGGC 2467	TCATTTTGCGCCATTCACCCCGGTGCCCTGAGAATGCCTTCTTCTTGGACCACGTGCGCG 2407	GGAGGAAGGCAAGAGGAAGTGGGCAGCCCAGACCATCCGTCGACTCATCCGTGGCT 2347	TTCTCCGGGTGAAGCGATCAGCCATCTGTATCCAGTCATGGTGGCGTGGCACACTGGGCC 2287	GGCAGAGTCTAGCCACCAAGATCCAGGGGGGCCTGGGAGGGGCTTTCATTGGCGACAGAAAT 2227	AGATCTTCATCCGCATTCCCCAAGACCTTATTTGCCACAGAGGACTCCCTGGAAGTCCGGC 2167	TGGCCGTGTTGGTCAGACCCTCGGCTACAAGCCAGAAGAGTACAAAATGGGCAGGACTA 2107 

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Db 118541 ATAGCCGCCTGCTCCGGCAACCAGACGACGGCGTCGAGGGCGTCAAGGACAAGCTGCTAAAG 118482
                                                                                                        Db 118601 CTCATCTCCGGAGAGAGTGGTTCCCGGCAAGAGGAGGCCTCCAAGAAGGTGCTGCAGTTC 118542
                                                                                                                                                                                                                    Db 118661 TTTGCGGTGACTGACAACGCCTTCCGTTCGCTGATCGAGGAGAACCGCGGCCAGTGCGTG 118602
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JOURNAL
                                                     437 TATIGCAGAGACCTGCCCAGCCCCTGAACGGGGTGGCGAGTGCGAGACCGCCTGTTGCAG
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                                                                                                                                            377 ATGATTTCTGGAGAGAGTGGGGCAGGCAAGACAGAGGCCACCAAGAGACTGCTCCAGTTC 436
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shir, E., Twomey, B., Wan, K.H., Zhang, R., Zieran, L.L. and Rubin, G.M.

Birect Submission

64-121, Lawrence Berkeley National Laboratory, One Cyclotron Road,
Berkeley, CA 94720, US

Sequence submitted by:
Lawrence Berkeley National Laboratory, MS 64-121

Earkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121

For further information about this sequence, including its location relationship to other sequences, please visit our sequence to bdgp@fruitfly.berkeley.edu.

Library locations: 11-34, 21-67, 44-36, 73-50, 92-76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Budaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endoptera; Endoptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

(CE 1 (Dases 1 to 268369)

RS (Chinker, S.E., George, R.A., Galle, R.E., Hoskins, R.A., Baxter, E., George, R.A., Chew, M., Doyle, C.M., Farfan, D.E., Chew, M., Doyle, C.M., Farfan, D.E., Lee, B., Lomotan, M.A., Mak, J., Mazda, P., Moshrefi, A.R., Moshrefi, M., Nixon, K., Pacleb, J.M., Park, S., Peiffer, B., Punch, E., Solir, E., Twomey, B., Wan, K. H., Zhang, R., Zieran, L.L. and Rubin, G.M. Unpublished (1997)

2 (bases 1 to 268369)

22 (bases 1 to 268369)

23 Sylrskas, R.R., Harris, N.L., Agbayani, A., Arcaina, T.T., Baxter, E., Planagan, J., Houston, K.A., Hummasti, S.R., Karra, K., Kearney, L., Solir, E., George, R.A., Galle, R.F., Hoskins, R.A., Blazej, R.G., Chavez, C., Chew, M., Doyle, C.M., Farfan, D.E., Chavez, C., Chew, M., Doyle, C.M., Farfan, D.E., Kim, S. H., Lee, B., Lomotan, M.A., Mak, J., Mazda, P., Moshrefi, A.R., Snir, E., Twomey, B., Wan, K.H., Zhang, R., Karra, K., Kearney, L., Moshrefi, A.R., Pacleb, J.M., Park, S., Pfeiffer, B., Punch, E., Snir, E., Twomey, B., Wan, K.H., Zhang, R., Zieran, L.L. and Rubin, G.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /Clone="Plb b603179 (D226), D806357 (D230), D803404 (D231), D806962 (D232), and D807291 (D240)", D806962 (D232), and D807291 (D240)", D806962 (D232), and D807291 (D240)", D806962 (D231) extends from bp 1 to bp 80,732 (D806) extends from bp 1,734 to bp 117,954 (D806) Extends from bp 82,734 to bp 117,954 (D806) (D230) extends from bp 88,745 to bp 169,482 (D806) (D230) extends from bp 127,117 to bp 209,427 (D806) (D232) extends from bp 194,759 to bp 268,369. "D807291 (D240) 71701 a 61029 c 61736 g 73903 t
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2527 116394	CCACACCCCCACCTGCCCTGAGAGAGGCCTCAGAACTGCTACGGGAACTGTGCATGAAGA	QY 2468 Db 116453	
2467 116454	CCTCATTTTTGCTTAACCTGAGGGGGCAACTGCCCCGGAATGTTCTGGACACCTCCTGGC	Qy 2408 Db 116513	
2407 116514	TCATTITGCGCCATTCACCCCGGTGCCCTGAGAATGCCTTCTTCTTGGACCACGTGCGCG	Qy 2348 Db 116573	
2347 116574	GGAGGAAGCCAGCCAAGAGGAAGTGGGCAGCCAGACCATCCGTCGACTCATCCGTGGCT	Qy 2288 Db 116633	
2287 116634	TTCTCCGGGTGAAGCGATCAGGCCATCTGTATCCAGTCATGGTGGCGTGGCGTGGCACACTGGGCCC	Qy 2228 Db 116693	
2227 116694	GGCAGAGTCTAGCCACCAAGATCCAGGCCGGCCTGGAAGGGGGCTTTCATTGGCGACAGAAAT	Qy 2168 Db 116753	
2167 116754	AGATCTTCATCCGATTCCCCAAGACCTTATTTGCCACAGAGGACTCCCTGGAAGTCCGGC	Qy 2108 Db 116813	
2107 116814	TGGCCGTGTTGGTCAGACACCTCGGCTACAAGCCAGAAGAGGTACAAAATGGGCAGGACTA	Oy 2048 Db 116873	
2047 116874	AGTCACTGTGCCCAGAGACATGGCCCATGTGGGCAGGACGGCCCCAGGATGGTG	Qy 1994 Db 116933	
1993 116934	GCGTGCGCAGAGCTGGCTTTGCCTATCGTCGCAAATATGAGGCTTTCCTGCAGAGGTACA	Oy 1934 Db 116993	
1933 116994	GCTTTGATGAGGTGCTCATCCGACATCAGGTGAAGTACCTGGGACTGATGGAGAATCTGC	Qy 1874 Db 117053	
1873 117054	GGTCTAAGGAGCCTGCCTATATCCGGTGCATCAAGCCAACGACGCCAAGCAGCCGGGTC	Qy 1814 Db 117113	
1813 117114	GCCCAG-GACGGTGGCCACCCAGTTCAAGATGAGCCTCCTGCAGGTCGTGGAGATCCTGA	Qy 1755 Db 117173	
1754 117174	GCTCAATGAACCCCATCATGGCCCAGTGCTTTGACAAGAGTGAGCTCAGTGACAAGAAGC	Qy 1695 Db 117233	
1694 117234	CTGGGTTTCTGGATAAAACAATGACCTCCTCTTCCGGAACCTGAAGGAGACCATGTGCA 	Qy 1635 Db 117293	
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1574 117354	CTGTCAAGCCCCACCCTCACCTTCCTGACGCACAAGCTCGCTGACCAGAAAGACCAGGAAAT	Qy 1515 Db 117413	

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2588 AGGCGGTGGCTAGTGAAATTTTCAAGGGCAAGAAGGACAACTACCCCCAGAGTGTCCCCCA 2647

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                                                                                      Db 116033 CGAACCACAACGACCTGATGGTCATCCGCATACCGCTCGACCTGAAAAAGGACAAGG 115974
                                                                                                                                                                             Db 116093 ACGGCAAGACCTACAAGCAGAAGCACCGCCTGCCGCTAGACAAGATCGACTTCACGCTGA 116034
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                                2936 GAGATGTGGTGCTGCAGAGTGATCATGTGATCGAG 2970
                                                                                                                    2876 GTAGCCTGAGTGATAGCCTATTTGTGCTTCACGTGCAGCGTGAAGAACAACAAGCAGAAGG 2935
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Compugen Ltd
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Human shear stress	Drosophila melanog	Drosophila melanog	Drosophila melanog	Drosophila melanog	Human polynucleoti	DNA encoding novel	DNA encoding novel	Human polynucleoti	Description	

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AAH99691 ABL12023
ABV22140
AAH98321 AAC77011
AAT34291
ABN59632
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AAS67617
AAT35761
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AAK52272
AAK53256
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AAK52971
AAK51987
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AAF16208
AAH34495
AAC76860
ABN96860
AAS84797
AAS94850
AAF32774
ABK52205
AAS40998
AAS40995

## ALIGNMENTS

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RESULT 1
AAI59147
  21-JAN-2000;
25-APR-2000;
09-JUL-2000;
19-JUL-2000;
19-JUL-2000;
14-SEP-2000;
19-OCT-2000;
                                                                                                                                                                                                                         Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
                                                                                                                                                  WO200153312-A1
                                                                                                                                                                                                             chemokinetic;
                                                                                                                                                                                                                                                                                   Human polynucleotide SEQ ID NO 1350
                                                                                                                                                                                                                                                                                                                                       AAI59147;
                                                                                                                                                                                                                                                                                                                                                               AAI59147 standard; cDNA; 4202
                                                                                                26-DEC-2000; 2000WO-US34263
                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                             22-OCT-2001 (first entry)
                                                                                                                          26-JUL-2001.
                                                                                                                                                                                                   leukaemia;
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2000US-0488725.
2000US-0552317.
2000US-05598042.
2000US-0620312.
2000US-0653450.
2000US-0662191.
2000US-0693036.
                                                                                                                                                                                                              thrombolytic; drug screening; arthritis; inflammation;
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29-NOV-2000; 2000US-0727344.

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The invention relates to human nucleic acids (AAI57798-AAI61369) and CCC the encoded polypeptides (AAM38642-AAM4213) with nootropic (CCC impunosuppressant and cytostatic accivity. The polypucleotides are useful CCC in gene therapy. A composition containing a polypeptide or polypucleotide (CCC system, such as peripheral nervous injuries, peripheral nervous containing a polypeptide or polypucleotide (CCC) localised neuropathies and central nervous system disease, such as CCC Alteral sclerosis, and Shy-Drager Syndrome, other uses include the CCC utilisation of the activity, chancer disease, amyotrophic CCC and thrombolytic activity, chancer disease, imune system suspension, CCC assays for receptor activity, cancer diseases and therapy, drug screening, CCC Note: The sequence data for this patent did not form part of the printed CCC specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         524 ANTGCCANGACTCTCCGCAACGATAACTCCAGCCGGTTTGGAAAGTACATGGATGTGCAG 583
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Best Local Similarity 86.4%;
Matches 3116; Conservative
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P-PSDB; AAM39991.
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RESULT 2
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standard;

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AAS74358 sta AAS74358; 13-FEB-2002

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The invention relates to isolated polynucleotide (I) and CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC for identifying expressed genes. (I) is useful an ingene therapy techniques (II). The CC (II). The CC (III). The CC (III) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as CC disorders involving abstrant protein expression or biological activity of III). (II) are useful for generating partners are useful in medical CC disorders involving abstrant protein expression or biological activity of adaptostics, forensics, gene mapping, identification of mutations in CC and to produce other types of data and products dependent on DNA and CC specification, but was obtained in electronic format directly from WIPO xx at fip.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 2906; Conserva
162 AGAACCTCCGGCGGCGGCTCCGGGAGAACCTCATTTATACCTACATCGGTCCTGTCCTAG 221
                                                                                                       102 GGGTAGGGGTGCAGGACTTTGTCCTGGTGGAGAAATTTCACCAGTGAGGCTGCCTTCATTG 161
                                                                                                                                                                                                                                       Sequence 3392 BP; 775 A; 993 C; 999 G; 625 T; 0 other;
                                                                                            94 GGTTGGGGGTGCAGGATTTCGTGCTGCTGGAGAACTTCACCAGGGAGGCCGCCTTCATCG
                                                                                                                                      New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations blodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID No 10162; 103pp; English.
                                              AGAACCTACGGCGGCGATTTCGGGAGAATCTCATCTACACCTACATTGGCCCCGTCCTGG
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding novel human diagnostic protein #10162.
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DB; ABG10171.
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86.5%; Pred. No. 0;
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2 TGCAGCAGCTCTTCATCGAGCTGACTCTCAAGTCGGAGCAGGAGGAGTACGAGGCTGACTCTCAAGTCGGAGCAGGAGGAGTACGAGGCTGAGGCTGAGTCGGAGCAGGAGGAGTACGAGGCTG 4 TGCAGCAGCTCTTCATCGAACTCCCGCTCAAGTCGGAGCAGGAGGAATACGAGGCAG	12 TTGAAGTGTTTCAGCATAACAGCTTCGAGCAGTTCTGCACCTCCLGGATATTTATGGCT 12:	** AUGUTGAGAGCCCCAGCTGGCGAAGCACCACGGTTCTTGGGCTCCTGGACATTTACGGC  ACGTGGAGAGCCCCAGCTGGCGGACCACCACGGTTCTTCGCCCTTCTTGGACATTTACGGC  ACGTGGAGAGCCCCAGCTGGCGGACCACCACGGTTCTTCTCCCCTTTTTTTT		)54 TCCTGAGCCCGCTGAACCTGGAACA	194 AAGGCTCGACGCTGCGAGAAGCCCTGACACACAGGAAGATCATCG 195 TCCTGAGCCCACTGAACCCTTGAACAGGAAGATCATCG	34 GCAATGCCCAGGTCACCACCGAGAACCAGCTCAAGTATCTGACCAGGC 02 AAGGTACAACATTAGGGAAGCCTGAGCCACAGGAACCAGGC 1111	10 A HAAGCATCGTGGCCAGCGTCCTTCATTTGGGCAACATCCACTTTGCTGCACCTTGCTGCCAACGAGCACATCTTGCTGAACGAGCAACAACAACAACAACAACAACAACAACAACAA	182 TOAGCATCGTGGCCAGCGTCCTACATCTGGGCAACATCTGGGTGTGATGAGGACCTGC 87	CGTCAGGAAGGCTCTGACAGTCATTGACTTCACTGAGGATGAAGTGGAGGAC	GTACCTGGTGAAGGGCCAGTGTGCCAAAGTCTC GGTTATGAGGAAGGCCTCTCTCTCTCTCTCTCTCTCTCTC	762 TGTACCTGGTGAAGGGCCAGGTGTGCAAGGCTCCAGCAACCCCCAAGGCTACC 7	A MONGGEGCGAGGAGGAGGACTCTCCGCTCGGCTGGGCTTGGAACGGAACGGAACGCCCAGĀGCTAGAGGAACGGAAC	CACGAGTGGTGCACCAGAATCATGGGGAGCGGAACTTCCACATCTTTACCAGCTACTGG 70	42 CCCGGGTGGTGCCACCAAAATCATGGAAAATCATGGAAAATCATGGAAAAAGT 63	FIGGAGGCCACATTCTCAGTTACCTCCTGGAAAAG	514 GAAATGCCAAGACCCTCCGGAACGATAACTCCAGCCGGTTTTGGAAAGTACATGGATGTGC 581	ACGCGGAGGTGCCGTGCGGGACCGGCTGCTACAGAGCAACCC	162 AACGGGGTGGCCAGTGCGAGACCGCCTGTTGCAGAGACCCCGCCTGCCCAGCCCC	394 GCAAGACCGAAGCCACCAAGAAGCTGCTGCAGAGAGAGACCTGCCCAGCCCCTG 461	CANGACAGAGGCCACCAAGAGACTCCTTCCTCCTCTCTCTCTC	334 GAGCACTGCGCACGCACCTGACCACTGATGATTTCTGGAGAGAGTGGGGCAG 4	342 CCCCTCAGCTTCTATGAAGTGCCCCCTCACCTGTTTGCCGTGGCGGACACTGTTTACC	274 CTCGTGTCAGTTTCTATGAAGTACCACCTCATTTGTTTGCAGTGGCTGACACTGTATACC 2	282 GTGGTGTC

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       GAGCTACCCCATGAGTGGGCCAGGCCGGGCCACCACCAATAGAAAAGCAGAGGCCTGAGC
                                                          GCGTGAAGACAACAAGCAGAAGGGAGATGTGGTGCTGCAGAGTGATCATGTGATCGAGAC
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RESULT 3
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ID AAS7
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AC AAS7
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DT 13-F
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DE DNA human

13-FEB-2002 (first entry)

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The invention relates to isolated polynucleotide (I) and CC polymeptide (II) sequences. (I) is useful as hybridisation probes. CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags cor identifying expressed genes. (I) is useful in gene therapy techniques CC in the common activity of (II) of the transition of (II). The common activity of (II) or to treat disease states involving CC quantitating a polypeptide in tissue, as molecular weight markers and as food supplement. (II) and its binding partners are useful in medical or CC insigning of sites expressing (II). (I) and (II) are useful for treating CC disgressing forensics, gene mapping, identification or biological activity. CC and to produce other types of data and products dependent on the color of sequences. Ass64197-Ass94564 represent novel human and CC specification, but was obtained in electronic format directly from WIPO.
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Matches 1847; Conservative
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Best Local
771 TGAAGGGCCAGTGTGCCAAGGTCTCCTCCATCAACGACAAGAGTGACTGGAAGGTTATGA 830
                                                        362 AGGAGGAGACTCTTCGGAGGCTGGGGCTTGGAACGCGCAGAGCTACCTGTACCTGG 421
                                                                        711 AGGAGGACACTCTCCGTCGGCTGGGCTTGGAACGGAACCCCCAGAGCTACTTGTACCTGG 770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations blodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID No 10163; 103pp; English.
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P-PSDB; ABG10172.
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23-AUG-2000; 2000US-0649167.
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81.7%; Pred. No. 0;
/ative 0; Mismatches
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Best Local Similarity
Matches 1267; Conser
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14-SEP-2000;
19-OCT-2000;
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
                                                                                                                                                                                                                                                                   The invention relates to human nucleic acids (AAI57798-AAI61369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system disease, such as alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin, hinhibin activity, chemotactic/chemokinetic activity, hamoostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhao
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Wang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel nucleic acids and polypeptides, useful such as central nervous system injuries -
                                                                                                                                                                                                         Sequence 1727
                                                                                                                                                                                                                                 specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-NOV-2000;
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                                                                                                 GCCCTGGGCAGTGACGGGGTTCGAGTGACCATGGAGAGCGCCTTGACTGCCCGAGACCGG 103
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QA,
            AACCTCCGGCGGTTCCGGGAGAACCTCATTTATACCTACATCGGTCCTAGTC
                                                           GTAGGGGTGCAGGACTTTGTCCTGCTGGAGAATTTCACCAGTGAGGCTGCCTTCATTGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001-442253/47.
DB; AAM41777.
                                                GTGGGGGTGCAGGATTTCGTGCTGCTGGAGAACTTCACCAGCGAGGCCGCCTTCATCGAG
AACCTGCGGCGATTTCGGGAGAATCTCATCTACACCTACATTGGCCCCGTCCTGGTC
                                                                                                                                                                                                                                           disorders.
The sequence
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Wang Z,
Zhou P,
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2000US-0662191.
2000US-0693036.
2000US-0727344.
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2000US-0552317.
2000US-0598042.
2000US-0620312.
                                                                                                                                                       Conservative
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Wehrman T, X
, Goodrich R,
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Xu C, Xue
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0; Mismatches
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167; Indels
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Yang
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GAAGTGTTTCAGCATAACAGCTTCGAGCAGTTCTGCATCAACTACTGCAATGAGAAGCTG
                                                        GCTGAGAGCCCCAGCTGCCGAAGCACCACGGTTCTTGGGCTCCTGGACATTTACGGCTTT 1243
                                                                                                   TACAGCCGGACATTCACCTGGCTGGTCAGAAAGATCAATAGGTCACTGGCCTCTAAGGAC
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                                                                                                                                                                                GECTCGACGCTGCGAGAAGCCCTGACACACAGGAAGATCATCGCCAAGGGGGAGGAGCTC
                                                                                                                                                                                                                          AATGCCCAGGTCAGCAGCGAGAACCAGCTCAAGTATCTGACCAGGCTCCTCAGCGTGGAA
                                                                                                                                                                                                                                       AATGCCCAGGTTACTACTGAGAACCAGCTCAAATATCTGACCAGGCTCCTTGGTGTGGAA 1003
                                                                                                                                                                                                                                                                    AGCATCGTGGCCAGCGTCCTACATCTGGGCAACATCCACTTTGCTGCTGACGAGGACAGC
                                                                                                                                                                                                                                                                                                                           GTTATGAGGAAGGCGCTGTCCGTCATTGACTTCACTGAGGATGAAGTGGAGGACTTGCTC
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                                                                                                                                                                                                                                                                                                                GTCGTCAGGAAGGCTCTGACAGTCATTGATTTCACCGAGGATGAAGTGGAGGACCTGCTG
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106 AGGGGTGCAGGACTTTGTCCTGCTGGAGAATTTCACCAGTGAGGCTGCCTTCATTGAGAA

CATGGCCAGTTTTAATTCCCAACTGAAAATGGAGACGGGCCTGCACGAGCGTGATCGTGC 175

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Best Local Similarity
                                                                                                 Matches 1708;
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                                                                                                                                                                                                 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and insecticides, theractions in higher eukaryotes for the development of discloses genomic DNA sequences (ABL016176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB5737-ABB72072).

The sequence data for this patent did not form part of the printed at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 10126; 21pp + Sequence Listing; English.
                                                      46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated nucleic acid genes from Drosophila and interactions -
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11-JUL-2000; 2000US-0614150;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila; developmental biology; cell signalling; insecticide;
pharmaceutical; gene; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-MAR-2002 (first entry)
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CCTGGGCAGTGACGGGGTTCGAGTGACCATGGAGAGCGCCTTGACTGCCCGAGACCGGGT
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                                                                                                                                                                  3406 BP; 885 A; 893 C; 924 G; 704 T; 0 other;
                                                                                       Conservative
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                                                                                                            23.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          detection reagent for detecting 1000 or more
for elucidating cell signalling and cell-cell
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                                                                     Score 875.2; DB 23;
Pred. No. 4e-236;
0; Mismatches 1183;
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                                                                     Indels
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                                                                53; Gaps
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1245 1281	1186 TGAGAGCCCCAGCTGGCGAAGCACCACGGTTCTTGGGCTCCTGGACATTTACGGCTTTGA	
1185 1230	1126 CAGCCGGACATTCACCTGGCTGGTCAGAAAGATCAATAGGTCACTGGCCTCTAAGGACGC	
1125 1170	1066 GAGCCCACTGAACCTTGAACAGGCGGCATATGCAAGGGATGCGCTTGCCAAGGCTGTGTA	
1065 1110	1006 TACAACACTTAGGGAAGCCCTGACCCACAGGAAGATCATCGCCAAGGGGGAAGAGCTCCT	
1005 1050	946 TGCCCAGGTTACTACTGAGAACCAGCTCAAATATCTGACCAGGCTCCTTGGTGTGGAAGG	
945 990	886 CATCGTGGCCAGCGTCCTACATCTGGGCAACATCCACTTTGCTGCTGACGAGGACAGCAA	
885 933	826 TATGAGGAAGGCGCTGTCCGTCATTGACTTCACTGAGGATGAAGTGGAGGACTTGCTCAG	
825 873	766 CCTGGTGAAGGGCCAGTGTGCCAAGGTCTCCTCCATCAACGACAAGAGTGACTGGAAGGT	
765 813	706 GGGCGAGGAGACTCTCCGTCGGCTGGGCTTGGAACGGAACCCCCAGAGCTACTTGTA	
705 753	646 GGTGGTGCACCAAAATCACGGAGAGCGGAACTTCCACGTCTTTTACCAGCTACTGGAGGG	
645 693	586 TGACTTCAAGGGTGCCCCCGTGGGAGGCCACATTCTCAGTTACCTCCTGGAAAAGTCCCG 	
585 633	526 TGCCAAGACTCTCCGCAACGATAACTCCAGCCGGTTTGGAAAGTACATGGATGTGCAGTT	
525 573	466 GGGTGGCGCAGTGCGAGACCCCCCTGTTGCAGAGCAACCCCCGTGTTAGAGGCCCTTTGGGAA	
465 513	406 GACAGAGGCCACCAAGAGACTGCTCCAGTTCTATGCAGAGACCTGCCCAGCCCCTGAACG	
405 453	346 ACTTCGTACTGAGCGTCGGGACCAGGCAGTGATGATTTCTGGAGAGAGTGGGGCAGGCA	
345 393	286 TGTCAGTTTCTATGAAGTACCACCTCATTTGTTTGCAGTGGCTGACACTGTATACCGGGC	
285	CTACAGATCTA	
225 273	CGGCGGCGGTTCCGGGAGAAC       }AAGAAGCG	
235	176 TGGAGTCCAGGACTTTGTGCTCCTCGAGAACTACCAGAGCGAAGAAGCCTTCATCGGGAA	

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Qy γQ Ъ Qy Qy Ъ Qy В Qy В QΥ Вр Š В Qy 밁 δÃ В Qy В Qy В Qy 망 δÃ 밁 Qy B δō DЬ Qy 망 밁 B В Qy 1402 2302 2182 2062 1942 1905 1762 1726 1642 1606 1522 1486 1426 1246 1845 CAAGCCAAACGACGCCAAGCAGCCGGGTCGCTTTGATGAGGTGCTCATCCGACATCAGGT TTATGCTGGAGAGGTGACCTACAGTGTGACTGGGTTTCTGGATAAAAACAATGACCTCCT 1665 CAAGCTCGCTGACCAGAAGACCAGGAAATCCCCTAGACCGAGGGGAGTTCCGCCTTCTGCA 1605 CGCGTGGGAACCTGTCCAGTACTTCAACAACAAGATCATGTGACCTGGTAGAGGAGAA 1425 CCAGTCATGGTGGCGTGGCACACTGGGCCGGAGGAGGCCAAGAGGGAAGTGGGCAGC 2318 CATGTGGGCAGGACGGCCCCAGGATGGTGTGGCCGTGTTGGTCAGACACCTCGGCTACAA CAAATATGAGGCTTTCCTGCAGAGGTACAAGTCACTGTGCCCAGAGACATGGCC-----GAAGTACCTGGGACTGATGGAGAATCTGCGCGTGCGCAGAGCTGGCTTTGCCTATCGTCG CTTCCGGAACCTGAAGGAGACCATGTGCAGCTCAATGAACCCCATCATGGCCCAGTGCTT 1725 CGAAAAGGCGCCCCCCCCCACATCAAGAAAATCATGCTGCGCGATGAGTTCCGCTTGGTGCA TAAGACCTTCCTTGAGAAGCTCACCCAGAAATTGGCCCAGCACCACCACTACGTTTGCCA CCTGACCTTTCTGGAGAAAGTTGGAGGACACTGTCAAGCCCCACCCTCACTTCCTGACGCA 1545 GTTCAAGGGCATCATCTCCATCTTGGATGAAGAGTGCCTGCGTCCTGGGGAGGCCACGGA 1485 GCAGAGCTATTGTCGCCGAAAGTTGGCACAGCAGGCGGCCAAGAAGCGCAGGGAGGCCGC CTGGAGGGGCTTTCATTGGCGACAGAAATTTCTCCGGGTGAAGCGATCAGCCATCTGTAT CGATACGGAGGATGCCTACCAGGAGAAGAACATGAGATAGCGGCCATCATCCAGGCCCA TGCCACAGAGGACTCCCTGGAAGTCCGGCGGCAGGAGTCTAGCCAACAAGATCCAGGCGGC GCCAGAAGAGTACAAAATGGGCAGGACTAAGATCTTCATCCGATTCCCCAAGACCTTATT CAAGTACCTTGGCCTGATGGAGAATCTGCGTGTGAGGCGAGCTGGTTTCGCCTACCGACG CAAGCCAAACGACCTGCAGACTGCCAACGTCTTCAACGATGAGTTGGTACTGCACCAGGT GTTCAGGGATCTAAAGGAGACCCTCAGCAAGGCTGGCAACGGCATTGTGAGGAACTGCTT CTATGCCGGCGAGGTCACCTACAGTGTCAATGGATTCCTGGACAAGAACAACGACCTGTT GCACAAGGGCATCATCTCCATACTGGACGAGGAGTGCTTGCGACCAGGAGAGCCCACGGA CGAGGAAAAGTACAGGGTGGGCGAGACGAAACTATTCATCCGCTGGCCGAGAACCTTGTT CAAGGGTCCCGGTGGCCCGAAAGCGGGTGTCCAGCAGCTGGTGAAAGATTTGGGCTGGGA 2121 1641 1581 1521 1701 2061 1964 1904 1761 2361 2138 1941 2181 2018 2001

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RESULT 6
ABL04915
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XW Dros
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XX Dros
XW Phar
XX PA
PR 23-M
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  23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                   23-MAR-2001; 2001WO-US09231
                                                                                       W0200171042-A2
                                                                                                     Drosophila melanogaster
                                                                                                            Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical; gene; ss.
                                                                                                                                             Drosophila melanogaster expressed polynucleotide SEQ ID NO 9227
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                                                                                                                                                                                                                                                                                                                  CATACCGCTCGACCTGAAAAAGGACAAGGGCGACTTGATTCTGATCATTCCGCGCATAAT 3021
                                                                                                                                                                                                                                                                                                                                   CGTGCAGCGTGAAGACAACAAGCAGAAGGGAGATGTGGTGGTGCTGCAGAGTGATCATGTGAT
                                                                                                                                                                                                                                                                                                                                                                                                             GCTGAGCAACAAGGCTATATATGTCCTCGACGGCAAGACCTACAAGCAGAAGCACCGCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CGGCATCCTTCACCGCCTGCACCGTCTCCACTTGGCCAGGATCTACCGCCTTAAACTGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGATAAGATTCGTGCCTTTATCAAGGCCTTCATCACCCGGAACGATGCCCCGAATGGCTT 2421
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Query Match
Best Local Sim.
Matches 1700;
605 GTGGGAGGCCACATTCTCAGTTACCTCCTGGAAAAGTCCCGGGTGGTGCACCAAAATCAC
                                                                                             536 GACAACTCCTCGCGGTTCGGCAAGTACATGGACATCCAGTTCGATTTCAAAGGAGCTCCG 595
                                                                                                                545 GATAACTCCAGCCGGTTTGGAAAGTACATGGATGTGCAGGTTTGACTTCAAGGGTGCCCCC
                                                                                                                                                     476 AAGCTGCTAAAGAGCAATCCCCGTGCTGGAGGCCTTCGGCAATGCCCAAGACAAACCGCAAT 535
                                                                                                                                                                    485 CGCCTGTTGCAGAGCAACCCCGTGTTAGAGGCCTTTGGGAATGCCAAGACTCTCCGCAAC 544
                                                                                                                                                                                                         416 GTGCTGCAGTTCATAGCCGCCTGCTCCGGCAACCAGACGACGTCGAGGGCGTCAAGGAC 475
                                                                                                                                                                                                                                                                356 GGCCAGTGCGTCATCTCCGGAGAGAGTGGTTCCGGCAAGACAGAGGCCTCCAAGAAG
                                                                                                                                                                                                                                                                                305 CCACCTCATTTGTTTGCAGTGGCTGACACTGTATACCGGGCACTTCGTACTGAGCGTCGG 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                        245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and insecticides, therapeutics in higher eukaryotes for the development of discloses genomic DNA sequences (ABLIG176 ABL30511, expressed DNA sequences (ABLIG176 ABL30511, expressed DNA Sequences (ABLIG175) and the encoded proteins The sequence data for this patent did not form part of the printed at fftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   185 GAGAACCTCATTTATACCTACATCGGTCCTGTCCTAGTCTCTGTCAATCCCTACCGAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        138 CTCCTCGAGAACTACCAGAGCGAAGAAGCCTTCATCGGGAATCTGAAGAAGCG-----
                                         ATCGGAGGCAACATCCTAAACTATCTGCTGGAAAAGTCGCGAGTGGTGGCTCAAATGGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78 CAACTGAAAATGGAGACGGGCCTGCACGAGCGTGATCGTGCTGGAGTCCAGGACTTTGTG 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 CGAGTGACCATGGAGAGCGCCTTGACTGCCCGAGAGCCGGGTAGGGGTGCAGGACTTTGTC 124
                                                                                                                                                                                                                               CTGCTCCAGTTCTATGCAGAGACCTGCCCAGCCCCTGAACGGGGTGGCGCAGTGCCGAGAC 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 9227; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid detection reagent for detecting genes from Drosophila and for elucidating cell signalling
                                                                                                                                                                                                                                                                                                                      CCCCACACATCTTTGCGGTGACTGACAACGCCTTCCGTTCGCTGATCGAGGAGAACCGC
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1803 1783	1745 GACAAGAAGCGGCCAG-GACGGTGGCCACCCAGTTCAAGATGAGCCTCCTGCAGCTCGTG
1744 1723	1685 ACCATGTGCAGCTCAATGAACCCCATCATGGCCCAGTGCTTTGACAAGAGTGAGCTCAGT
1684 1663	1625 TACAGTGTGACTGGGTTTCTGGATAAAACAATGACCTCCTCTTCCGGAACCTGAAGGAG
162 <b>4</b> 1603	1565 ACCAGGAAATCCCTAGACCGAGGGGAGTTCCGCCTTCTGCATTATGCTGGAGAGGTGACC
1564 1543	1505 TTGGAGGACACTGTCAAGCCCCACCCTCACTTCCTGACGCACAAGCTCGCTGACCAGAAG
1504 1483	1445 ATCTTGGATGAAGAGTGCCTGCGTCCTGGGGAGGCCACGGACCTGACCTTTCTGGAGAAG
1444 1423	1385 TACTTCAACAACAAGATCATCTGTGACCTGGTAGAGGGAGAAGTTCAAGGGCATCATCTCC
1384 1363	1325 ACTCTCAAGTCGGAGCAGGAGGATACGAGGCTGAGGGCATCGCGTGGGAACCTGTCCAG
1324 1303	1265 TTCGAGCAGTTCTGCATCAACTACTGCAATGAGAAGCTGCAGCAGCTCTTCATCGAGCTG
1264 1243	1205 AGCACCACGGTTCTTGGGCTCCTGGACATTTACGGCTTTGAAGTGTTTCAGCATAACAGC
1204 1186	1145 CTGGTCAGAAAGATCAATAGGTCACTGGCCTCTAAGGACGCTGAGAGCCCCAGCTGGCGA
1144 1132	1085 CAGGCGGCATATGCAAGGGATGCGCTTGCCAAGGCTGTGTACAGCCGGACATTCACCTGG
1084 1072	1025 CTGACCCACAGGAAGATCATCGCCAAGGGGGAAGAGCTCCTGAGCCCACTGAACCTTGAA
1024 1012	965 AACCAGCTCAAATATCTGACCAGGCTCCTTGGTGTGGAAGGTACAACACTTAGGGAAGCC
964 952	905 CATCTGGGCAACATCCACTTTGCTGCTGACGAGGACAGCAATGCCCAGGTTACTACTGAG 
904 895	845 GTCATTGACTTCACTGAGGATGAAGTGGAGGACTTGCTCAGCATCGTGGCCAGCGTCCTA
844 835	785 GCCAAGGTCTCCTCCATCAACGACAAGAGTGACTGGAAGGTTATGAGGAAGGCGCTGTCC
784 775	725 CGTCGGCTGGGCTTGGAACGGAACCCCCAGAGCTACTTGTACCTGGTGAAGGGCCAGTGT
715	656 GGCGAGCGCAACTTCCACATCTTCTACCAACTCTTGGCCGGCGCCGACGAGGCCCCTTCTG

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                                                                                                                                                                                                 The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                  The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and insecticides, therapeutics and pharmaceutics for the development of discloses genomic DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
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                                                                                                                                                                           Sequence 6483 BP; 1768 A; 1550 C; 1583 G; 1582 T; 0 other:
                                                                                               317 TTTGCAGTGGGTGACACTGTATACCGGGGCACTTCGTACTGAGGGTCGGGACCAGGCAGTG 376
                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 10123; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic a
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11-JUL-2000;
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pharmaceutical; gene; ds.
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TATGCAGAGACCTGGCCAGCCCCTGAACGGGGTGGGGCAGTGCGAGACCGCCTGTTGCAG
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                                 CTCATCTCCGGAGAGAGTGGTTCCGGCAAGACAGAGGCCTCCAAGAAGGTGCTGCAGTTC
                                               ATGATTTCTGGAGAGAGTGGGGCAGGCAGGAGAGAGGGCCACCAAGAGACTGCTCCAGTTC
                                                                             TTTGCGGTGACTGACAACGCCTTCCGTTCGCTGATCGAGGAGAACCGCGGCCAGTGCGTG 2297
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG1840-ABLIG1855) and the encoded proteins
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIFO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                          arteriosclerosis;
                                                                                                                                                                      Human; shear stress-response
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                                CGGGTGGTGCACCAAAATCACGGAGAGGGGAACTTCCACGTCTTTTACCAGCTACTGGAG
                                                                         TTTGACTTCAAGGGTGCCCCCGTGGGAGGCCACATTCTCAGTTACCTCCTGGAAAAGTCC
                                                                                                        AATGCCAAGACTCTCCGCAACGATAACTCCAGCCGGTTTGGAAAGTACATGGATGTGCAG
                                                                                                                                                   GTAGGGGTGCAGGACTTTGTCCTGCTGGAGAATTTCACCAGTGAGGCTGCCTTCATTGAG
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DB; AAB90827.
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 GGGGGCGAGGAGGACTCTCCGTCGGCTGGGCTTGGAACGGAACCCCCAGAGCTACTTG
                    CGAGTGGTGCACCAGAATCATGGGGAGCGGAACTT-CACATCTTCTACCAGCTGCTGGAG
                                                                TTTGACTTCAAGGGTGCCCCCGTGGGTGGCCACATCCTCAGTTACCCCCTGGAAAAGTCA
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Sekine S,
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                                                                                                                                                                                The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and insecticides, therapeutics and pharmaceutics for the development of discloses genomic DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB5737-ABB72072).
                                                                                                                        The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                               Sequence 3874
                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 37252; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          New isolated nucleic acid
genes from Drosophila and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-656860/75.
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11-JUL-2000; 2000US-0614150
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                                                                                                                                                   GCGATGGTGTCCGTGTGCTGATCGAGGAAAAGAAATTCGCCCAGGACGTTAAGTACGGCC
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19-WAY-2000
07-JUN-2000
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07-JUL-2000
07-JUL-2000
11-JUL-2000
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              2000US-0186350
2000US-0198174
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2000US-0216486
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Best Local Similarity 54.7
Matches 1169; Conservative
416 ACCAAGAGACTGCTCCAGTTCTATGCAGAGACCTGCCCAGCCCCTGAACGGGGTGGCGCA
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11-DEC-2000;
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05-JAN-2001;
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                                                             CGTTCCAGGGACACCTGCATCGTCATCTCAGGGGAGAGTGGGGCAGGGAAGACAGAAGCC
                                                                                     TATGAAGTACCACCTCATTTGTTTGCAGTGGCTGACACTGTATACCGGGGCACTTCGTACT
                                                                                                                                         TACCAGGAGCTGCCCCTGTATGGGCCTGAGGCCATCGCCAGGTACCAGGCCCGTGAGCTC
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2000US-0254097.

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Pred. No. 3.3e-132;
1; Mismatches 917; Indels 52;
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21 - OCT - 200

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            TGCCTGCGTCCTGGGGAGGCCACGGACCTGACCTTTCTGGAGAAGTTGGAGGACACTGTC
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17-DEC-2001 (first entry)

cDNA encoding novel human enzyme polypeptide #214.

Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase ligase; hyperproliferative disorder; immunodeficiency disorder; autoimmune disorder; neurological disorder; metabolic disorder; inflammatory disorder; cardiovascular disorder; reproductive disorder; blood-related disorder; infectious disorder; gene therapy; cytostatic; arthritic; nephrotropic; anticoagulant;

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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at the printed at the large of the printed and the printed and the printed and the printed at the pri
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54.7%;
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Pred. No. 7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .2e-132;
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                                                                                                                                                                                                                GACCGAGGGGAGTTCCGCCTTCTGCATTATGCTGGAGAGGTGACCTACAGTGTGACTGGG
                                                                                                                                                                                                                                                                                                                                                                       TGCCTGCGTCCTGGGGAGGCCACGGACCTGACCTTTCTGGAGAAGTTGGAGACACTGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATCATCTGTGACCTGGTAGAGGAGAAGTTCAAGGGCATCATCTCCATCTTGGATGAAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAGGAAGAGTACGAGCGCGAGGGCATCACCTGGCAGAGCGTTGAGTATTTCAACAACGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CACCAGGCAGTGACCGAGGCCATGAGGGTCATCGGCTTCAGTCCTGAAGAGGTGGAGTCT
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  GAAGCGGCCAGGACGGTGGCCACCCAGTTCAAGATGAGCCTCCTGCAGCTCGTGGAGATC
                                                                                                                  TTCATCGACAAGAACAGAGTTTCCTTCCAGGACTTCAAGCGGCTGCTGTACAACAGC
                                                                                                                                                                                          GGCCGA----GACTTCCGGATCAAGCACTATGCAGGGGACGTCACGTACTCCGTGGAAGGC
                                                                                                                                                                                                                                                                      CGCCATCACCTACACCAGCCGCCAGCTCTGCCCCACAGACAAGACCATGGAGTTT
                                                                                                                                                                                                                                                                                                            AAGCCCCACCCTCACTTCCTGACGCACAAGCTCGCTGACCAGAAGACCAGGAAATCCCCTA
                                                                                                                                                                                                                                                                                                                                                   TGCAGCTCTGCTGGCACCATCACTGACCGAATCTTCCTGCAGACCCTGGACACGCACCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GACAGCAATGCCCAGGTTACTACTGAGAACCAGCTCAAATATCTGACCAGGCTCCTTGGT
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                                      ACGGACCCCACTCTACGGGCCATGTGGCCGGACGGGCAGCAGGACATCACAGAGGTGACC
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                                                                          -GGCCCAGTGCTTTGACAAGAGTGAGCTCAGTGACAA
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Novel probe for use in assay identifying and/or isolating
                                  WPI; 2002-434908/46.
P-PSDB; AAU97544.
                                                         Thuring
                                                                  Stephens L,
                                                                              (BABR-) BABRAHAM INST.
(UYCA-) UNIV CAMBRIDGE TECH SERVICES
(LIMZ/) LIM Z.
                                                                                                               23-AUG-2000;
15-DEC-2000;
                                                                                                                                   23-AUG-2001; 2001WO-GB03791
                                                                                                                                                     07-MAR-2002
                                                                                                                                                                     WO200218946-A2
                                                                                                                                                                                                                                Human; phosphoinositide-binding protein; phosphatidyl acid; gene; phosphatidic acid; signal transduction; housekeeping; myosin-lF; 
                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                            DNA encoding human Myosin-1F protein MYO1F.
                                                                                                                                                                                                                                                                                 13-AUG-2002
                                                                                                                                                                                                                                                                                                          ABK52205 standard; DNA; 3617 BP
                                                                                                                                                                                                                                                                                                  ABK52205
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                                                                                                                                                                                                                                                                                                                                                           CAGAGTCTAGCCACCAAGATCCAGGCGGCCTGGAGGGGC 2208
                                                                                                                                                                                                                                                                                                                                                                          CTGTTCATCCGCTCACCCCGGACACTGGTCACACTGGAGCAGAGCCGAGCCCGCCTCATC
                                                                                                                                                                                                                                                                                                                                              CCCATCATTGTGCTGCTATTGCAGAAGGCATGGCGGGGC 2327
                                                                                                                                                                                                                                                                                                                                                                                                        ATCTTCATCCGATTACCCCAAGACCTTATTTGCCACAGAGGACTCCCTGGAAGTCCGGGGGG
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                                                          JWJF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGGAAGCTGGATGAGAACCACTGTCGCCACCAGGTCGCATACCTGGGGGCTGCTGGAGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGTCGCTTTGATGAGGTGCTCATCCGACATCAGGTGAAGTACCTGGGACTGATGGAGAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hawkins
                                                                                                             2000GB-0020833.
2000GB-0030637.
                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                       /*tag= a
/product= "Human myosin-1F protein MYO1F"
                                                                                                                                                                                                  Location/Qualifiers
41..3337
                                                                PΤ,
                                                              Holmes
       / method for
J PA- and/or
                                                             AB,
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  detecting, measuring, PIPn-binding protein
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                                                         Ktistakis
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Best Local Similarity
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The present invention relates to a new probe comprising or consisting of CC an immobilised phosphatidy acid derivative attached on to a solid CC support, or a phosphatidic acid (PA) functionalised solid support. The control of the invention is useful in an assay method for identifying a protein that binds to the probe. The invention is also cone type of phosphatidic acid and/or phosphatidic acid and/or isolating protein cC assay is also useful for detecting, measuring, identifying and/or isolating protein cC assay is also useful for detecting, measuring, identifying and/or phosphotiositide binding protein cC assay is also useful for detecting, measuring, identifying and/or the control of the phosphatidic acid and/or phosphotnositide-binding proteins in cc at test sample, to detect and/or measure the ability of an agent, applied test sample, to agonise or antagonise protein-probe binding protein-containing cd detect and/or measure the ability of an agent, applied to the probe, to consphoinosit or antagonist or antagonist or protein-probe binding. The probe is useful for cc identifying an agonist or antagonist or protein-probe binding. The probe is useful for identifying and in a single step high throughput screen of candidate componist and/or antagonist. The invention is also useful for identifying for probe is useful as an important research tool in fundamental research cc encodes the human myosin-IF protein MYOIF of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 133-134; 163pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sample, has immobilised phosphatidyl acid attached to solid support
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3617 BP; 809 A; 1103 C; 1073 G; 631 T; 1 other;

Matches 1149; 662 CACATCTACCTACCAGCTGCTGGAAGGGGCCTCCCAGGAGCAAAGGCAGAACCTGGGCCTC 482 AACCCGCTGCTCGAGGCCTTCGGCAACGCCAAGACTGTGCGCAACAACAATTCCAGCCGC 362 ATTAGTGGAGAGAGTGGAGCTGGGAAGACAGTGGCAGCCAAATATATCATGGGCTACATC 380 ATTICTGGAGAGAGTGGGGGAGGCAAGAGAGAGAGAGAGAGAGTGCTCCAGTTCTAT 302 242 182 ACCTACATCGGCTCTGTGCTCATCTCTGTAAACCCCCTTCAAGCAGATGCCCCTACTTCACC 140 ACCAGTGAGGCTGCCTTCATTGAGAACCTCCGGCGGCGGTTCCGGGAGAACCTCATTTAT 199 122 ATCACCGAAGACGCCATTGCCGCCAACCTCCGGAAGCGCTTCATGGACGACTACATCTTC 181 200 : TCCAACTTCTTGCTGGAGAAGTCCCGCGTGGTCATGCAAAATGAAAATGAGAGGAACTTC CTCAGTTACCTCCTGGAAAAGTCCCGGGTGGTGCACCAAAATCACGGAGGGGAGCTTC TTTGGAAAGTACATGGATGTGCAGTTTGACTTCAAGGGTGCCCCGTGGGAAGCCACATT TTTGGCAAGTACTTTGAGATCCAGTTCAGCCGAGGTGGGGAGCCAGATGGGGGCCAAGATC AACCCCGTGTTAGAGGCCTTTGGGAATGCCAAGACTCTCCGCAACGATAACTCCAGCCGG TCCAAGGTGTCTGGCGGAGGCGAGAAGGTCCAGCACGTCAAAGATATCATCCTGCAGTCC GCAGAGACCTGCCCAGCCCCTGAACGGGGTGGCGCAGTGCGAGACCGCCTGTTGCAGAGC 499 CGCCAGCATATGGAACGCTACCGTGGTGTCAGTTTCTATGAAGTACCACCTCATTTGTTT GCCCTCACGGACAACATGTACCGGAACATGCTTATCGACTGTGAGAACCAGTGTGTCATC GCAGTGGCTGACACTGTATACCGGGCACTTCGTACTGAGCGTCGGGACCAGGCAGTGATG GACCGTGAGATCGACCTCTATCAGGGCGCGCGCCCAGTATGAGAATCCTCCGCACATCTAC ACCTACATCGGTCCTGTCCTAGTCTCTGTCAATCCCTACCGAGACCTACAGATCTACAGC Conservative 12.68; 0; Mismatches Score 460.8; DB 24; Pred. No. 5e-119; 857; Indels Length 3617; 94; Gaps 661 679 601 559 481 421 361 379 301 259 241 8

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      The invention relates to the isolation of genes AAF32757-F32803 47 human secreted profesins AAB64349-B864594. The genes can be use generate fusion proteins by linking to the gene for the human immunoglobulin G Fc portion (SEQID1) for increasing the stabilit the fusion protein as compared to the human protein only. The gene for the human protein only.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparastitc; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human; secreted protein; ss.
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                                                                                                                       Isolated nucleic acid molecule encoding a human secreted protein used in preventing, treating or ameliorating a medical condition
                                                                                                                                                                      P-PSDB;
                                                                                                                                                                                                                                                                                            11-JUN-1999;
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                    862 GGATGAAGTGGAGGACGTGCTCAGCATCGTGGCCAGCGTCCTACATCTGGGCAACATCCA 921
                                                                                                                       1416 GAGGGATTTCAGCAGGTATAACTACCTGAGTCTGG---ATTCGGCCAAAGTGAATGGAGT 1360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CC conditions, e.g. by protein or gene therapy. The genes are isolated CC from a range of human tissues disclosed in the specification. The GC nucleic acids, proteins, antibodies and (ant)agonists are isolated CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast CC marrow, breast, gastrointestinal tract, liver, lung, or urogenital CC (b) immune disorders e.g. Addison's disease, altergies, autoimmune CC disease, multiple sclerosis, rehumatoid arthritis and uricerative CC colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) ce gellepsy; and (f) infectious diseases e.g. cerebral anoxia and XXX and parasitic infections.
                                                                              802 CAACGACAAGAGTGACTGGAAGGTTATGAGGAAGGCGCTGTCCCGTCATTGACTTCACTGA 861
                                                                                                                                                                                   1476 TGTGTTGTATCAGCTGCTCTGTGTGCCTCTGAAGAGCTCCTCAATAAACTTAAGCTTGA 1417
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 12.3%; Score 450.6; DB 22; Length 2263;
Matches 1083; Conservative 0; Mismatches 909; Indels 37; Gaps
                                                                                                                                                                                                                                                 1596 TGGCAAATATATGGATATTGAATTTGACTTTAAAGGCGATCCACTAGGAGGAGTAATAAG 1537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        202 CTACATGGGTCCTGTCCTAGTCTGTCAATCCCTACGGAGACCTACAGATCTACAGCCG 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2263 BP; 563 A; 529 C; 459 G; 712 T; 0 other;
                                                                                                                                                                                                                                                                                                                               TGGAAAGTACATGGATGTGCAGTTTGACTTCAAGGGTGCCCCCCGTGGGAGGCCACATTCT 621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGAGACCTGCCCAGCCCCTGAACGGGGTGGCGCAGTGCGAGACCGGCTGTTGCAGAGCAA 501
                                                                                                                                                                                                                                                                                                                                                                                                                                      AGCTGTTTGTGGAAAAGGAGCAGAAGTTAATCAAGTTAAAGAACAGCTTTTACAGTCCAA 1657
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83 GCAGAGGTACAAGTCACTGTGCCCAGAGACATGGCCCATGTGGGCAGGACGGCCCCAG	34 GGAGAACGTCCGAGAGGCAGAGCTTATCCTTTATCGTCGAAATATGAGGCTTTCCT 19	23	863	354 GAAAAACCTACAGAGCAAGAACCAAACTATTTTTTTTTT	803 GGAGATCCTGAGGTCTAACGCTCACAGTTCAAGGCATCCGTGGCCACTCTGAT	CAACCTGAAAAGGCCTTCCTTACTTTTTTTTTTTTTTTT	GAAGCGGCCACC		334 GGTGGAAGGATTCGTTGAGAAAAAAAAATGACCTTCTCTATCGAGACCTTGTCCCAAGCCAT 1689 1690 GTGGAGCTCAATGAACCACTTTTCTCTTATCGAGACCTTGTCCCAAGCCAT 475	TGTGACTGGGTTTCTGGATAAAAACAATGACCTCCTCTTCCGGAACCTGAACCACCACCACACCACACACA	594 CACGTCTCTGCCTCACAGCTGCTTCAGGATCCAGCATTATGCTTGCAAAACCTTCTT	1570 GAAATCCCTAGACCGAGGGGACTTCCGCCTTCTGCATTATTCCTCCATTGA 595	GAA	1516 TGTCAAGCCCCACCCTCACTTCCTCACCCTTCTTAGAAAAGCTGAACCAAGT 655	714 AGAGTGCCTCAGACCTGGCACAGTCATCATTCATTCATTC	1456 AGAGTGCCTGCGTCCTGGGCAGGCCAGCCAGCCAGCCATGCTGGATGA 715	774 TGCTATCATTTGTGACCTAATAGAAAATTACAATCATCATCTCCATCTTGGATGA 1455	1396 CAAGATCATCTGTGACCTGCTACACCACACTAGAACTGACTACATAAA 775	834 AGAGCAGGAGGAGTATATACGGGGAGCATATATACGGGAACCATGTCGAGGAACCTGTCCAGGAACAA 1395	1336 GGAGCAGGAGGATACGAGGCTGAGGCCTTACAGCAACTTACTCTTAAAGA 835	894 CATTATTAATTATTGTAACGAAAACCTCCTCATCGAGCTCTCAACTC 1335	1276 CTGCATCAACTACTGCAATGACAACGCTTTGAGCACTATGAGCACTTTGAGCACTATGAGCACTATGAGACAACGCTTTTGAGCACTATGAGACAACGCTTTTGAGCACTAAGGCACTATGAGACAACGCTTTTGAGCACTAAGGCACTATGAGACAACGCTTTTGAGCACTAAGGCACTATGAGAAACGCTTTTGAGCACTAAGGCACTATGAGAAACGCTTTTGAGCACTAAGGCACTATGAGAAACGCTTTTGAGCACTAAGGCACTATGAGAAACAAGCTTTTGAGCACTAAGGCACTATGAGAAACAAGCTTTTGAGCACTAAGGCACTATGAGAAACAAGCTTTTTGAGCACTAAGAAGAACAAGCTTTTGAGCACTATGAAGAAACAAGCTTTTGAGCACTATGAAGAACAAGCTTTTGAGAAACAAGCTTTTGAGCACTATAAACAAGCTTTTTGAGAAACAAGCTTTTTGAGAAACAAGCTTTTTAAGAACAAACA	954 CATGGGTGTTCTGGACATTTATGGCTTTTCAGCATTATCAGCATAACAGCTTCGAGCAGTT 1275	1216	999 AATCAATG	1156	1059	1096 T	b 1119 CCGAACAGTTGAGCCAACAGAGAAACTTGAACCAGTGAACAGGCGGCATA 1095	1036 G	Db 1179 TTAAAAGAAATTTGTGAATTGCCGCATTACCGCATTAGGGAAGCCCCTGACCCCACAG 1035	QY 977 -TATCTGACCAGGCTCTTTCCTTTTCCTTTTCCTTTTCCTTTTCCTTTTCCTTTT	1239 GTTCAAGCCCGAATCCCCCCCCCCCCCCCCCCCCCCCCC	Qy 922 CTTTGCTGCTGACGACGACGACGACGACGACGACGACGACGACGACGACG

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                                                                                                                                                                                                                                   composition comprising these polynucleotides are useful as a high throughput method for detecting altered expression of one or more polynucleotides in a sample. The polynucleotides can be used in the diagnosis of disorders associated with foam cell development such as atherosclerosis, cerebral stroke, and cardiovascular disorders such as coronary artery disease. The polynucleotide sequences can also be used as PCR primers and probes. The polynucleotides of the invention are also useful in gene therapy. AAS94746-AAS95021 represent the human polynucleotide sequences of the invention which are differentially expressed during foam cell differentiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2103
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                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to the isolation of human polynucleotide sequences that are differentially expressed during foam cell differentiation. The polynucleotide sequences of the invention or a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 156-158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Composition useful for diagnosis of conditions, disorders or diseases associated with atherosclerosis, comprises several polynucleotides that are differentially expressed in foam cell development -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shiffman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-APR-2000; 2000US-195106P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cardiovascular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human DNA sequence #105 expressed during foam cell differentiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAS94850 standard; DNA; 4760
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                                                                                                                       Local Similarity
nes 1119; Conserv
                                                                GACTTTGTCCTGCTGGAGAATTTCACCAGTGAGGCTGCCTTCATTGAGAAACCTCCGGCG 174
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                                       GGACGACATGGTGCTACTGTCCAAGATCACAGAGAACTCCATCGTGGAGAATCTGAAGAA 523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCGGTTCCGGGAGAACCTCATTTATACCTACATCGGTCCTGTCCTAGTCTCTGTCAATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        foam cell differentiation; atherosclerosis;
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                                                                                                                                                                                                  4760 BP;
                                                                                                                       Conservative
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                                                                                                                                                                                                1331 A; 1150 C; 1233 G; 1046 T; 0 other
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51.9%;
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0; Mismatches
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1243 TGAAGTGTTTCAGCATAACAGCTTCGAGCAGTTCTGCATCAACTACTGCAATGAGAAGCT
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                                                                                                                                                                                                                  CCACGTGACCCTCAACGTAGAGCAGGCCTGTTACACCCCGGGATGCGCCTCGCCAAGGCCCT
                                                                                                                                                                                                                                         CCTGAGCCCACTGAACCTTGAACAGGCGGCGCATATGCAAGGGATGCGCTTGCCAAGGCTGT 1122
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                                                           TGAAGAATACAACA - - -
                                                                                                                                      GCACGCCCGGGTCTTTGATTTCTTGGTAGATTCCATCAATAAAGCCATGGAGAAAGACCA
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                                                                                              CGCTGAGAGCCCCAGCTGGCGAAGCACCACGGTTCTTGGGCTCCTGGACATTTACGGCTT 1242
                                                                                                                                                                                                                                                                                                                                                                                                                    TACTACTGAGAACCAGCTCAAATATCTGACCAGGCTCCTTGGTGTGGAAGGTACAACACT 1014
                                                         TTGGCGTCCTAGACATCTATGGCTT
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                           2193 GGCGGCCTTGGAGGGGCTTTCATTGGCGACAGAAATTTCTCCGGGGTGAAGCGATCAGCC 2250
                                                        2450 TCTATTTCTTTTAGAAGAGATGAGAGAGAGAAAGTATGATGGGTATGCTCGAGTGATACA 2509
                                                                                  2133 CTTATTTGCCACAGAGGACTCCCTGGAAGTCCGGCGGCAGAGTCTAGCCACCAAGATCCA 2192
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ALIGNMENTS

## RESULT 1 US-08-938-105-2 ; NAME/KEY: ; LOCATION: US-08-938-105-2 STREET: 1700 Lincoln St., Suite 3500 CITY: Denver STATE: CO COUNTRY: U.S.A. ZIP: 80203 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 Sequence 2, Application US/08938105 Patent No. 6353151 GENERAL INFORMATION: Query Match Best Local ! Matches 534; TELEFAX: (303) 863-0223 INFORMATION FOR SEQ ID NO: ATTORNEY/AGENT INFORMATION: NAME: Crook, Wannell M. REGISTRATION UNMBER: 31,071 REFERENCE/DOCKET NUMBER: 3595 TELECOMMUNICATION INFORMATION: TELEPHONE: (303) 863-9700 NUMBER OF SEQUENCE. CORRESPONDENCE ADDRESS: CORRESPONDENCE Sheridan Ross P.C. PDRESSEE: Sheridan St., Su CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/938,105 FILING DATE: CLASSIFICATION: APPLICANT: Leinwand, Leslie A. APPLICANT: Vikstrom, Karen L. TITLE OF INVENTION: TRANSGENIC NUMBER OF SEQUENCES: 3 FEATURE: MOLECULE TYPE: CDNA SEQUENCE CHARACTERISTICS: LENGTH: 5661 base pairs y Match 4.18; Local Similarity 49.28; STRANDEDNESS: TOPOLOGY: lir TYPE: nucleic acid ADDRESSEE: SHELL, Conservative CDS 1..5661 linear single 2: 0; 3595-4 Score 149.4; DB 4; Pred. No. 8.2e-31; 0; Mismatches 516; MODEL FOR HEART FAILURE Indels Length 5661; 35; Gaps

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                                         TCAGTGTACGAGAAGATGTTCAACTGGATGGTGACACGCATCAACGCAACCCTGGAGACC 1347
                                                                                                       TATGTCACCAAGGGGCAGAGTGTACAGCAGGTGTACTATTCCATCGGGGCACTGGCCAAG
                                                               GCTGTGTACAGCCGGACATTCACCTGGCTGGTCAGAAAGATCAATAGGTCACTGGCCTCT 1177
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Sequence 2, Application US/09172422A

Patent No. 6300485
GENERAL INFORMATION:
APPLICANT: Adams, Arwen E.
APPLICANT: Chiu, Choi Ying
APPLICANT: Chiu, Choi Ying
APPLICANT: Gorman, Susan W.
APPLICANT: Leng, Song
APPLICANT: Leng, Song
APPLICANT: Sheffield, Val
APPLICANT: Welch, Juliet
TITLE OF INVENTION: CHANKEL-15 (CNGC-15) POLYNUCLEOTIDE GATED
TITLE OF INVENTION: COMPOSITIONS, METHODS, AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/172,422A
CURRENT FILING DATE: 1998-10-14
CURRENT FILING DATE: 1998-10-14
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LENGTH: 8473
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-172-422-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 2
US-09-172-422-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTATTCTATTACCTCCTGGCAGGAGCAAGTGAAGA 1285
                                           GTCTTTTACCAGCTACTGGAGGGGGGGGGGAGGAGGA 717
                                                                               AAATATCTACTGGAGAAGTCCAGACTCGTTTATCAGGAGCATAATGAACGGAACTATCAT 1250
                                                                                                                          AGTTACCTCCTGGAAAAGTCCCGGGTGGTGCACCAAAATCACGGAGAGCGGAACTTCCAC
                                                                                                                                                                     GGGAAGTTTATTCAAGTAAATTACCAGGAAACAGGCACTGTACTTGGTGCCTATGTTGAA 1190
                                                                                                                                                                                                    GGAAAGTACATGGATGTGCAGTTTGACTTCAAGGGTGCCCCCGTGGGAGGCCACATTCTC
                                                                                                                                                                                                                                                                CCAGTACTTGAGGCCTTTGGAAATGCAAAGACAGCTCATAATAACAATTCAAGTCGTTTT
                                                                                                                                                                                                                                                                                        CCCGTGTTAGAGGCCTTTGGGAATGCCAAGACTCTCGGCAACGATAACTCCAGCCGGTTT 562
                                                                                                                                                                                                                                                                                                                                                    GCTCTCAGTCAGAA---AGGATTTGCCAGTGGAGTAGAACAGATTATTCTTGGAGCTGGA 1070
                                                                                                                                                                                                                                                                                                                                                                                                                                             TCAGGAGAGAGTGGTTCTGGGAAGACTCAAAGCACAAACTTTCTTATTCACCACCTTACT 1013
                                                                                                                                                                                                                                                                                                                                                                                                GAGACCTGCCCAGCCCCTGAACGGGGTGGCGCAGTGCGAGACCGCCTGTTGCAGAGCAAC 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTGGAGAGAGTGGGGCAGGCAAGACAGAGGCCACCAAGAGACTGCTCCAGTTCTATGCA 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TACATCGGTCCTGTCCTAGTCTCTGTCAATCCCTACGAGACCTACAGATCTACAGCCGG
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                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 693 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 31-DEC-1996 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
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386 GGAGAGAGTGGGGCAGGCCAAGACAGAGGCCCACCAAGA 422
                                   102
                                                                                                   162 TATGTGAACTTGTACCATGGGTCACCCAAGGAAGACAACGAGCCGCATATCTTTGCGGTA 103
                                                                                                                                                                         222
                                                                                                                                                                                                                                             282
                                                                                                                                                                                                                                                                         146 GAGGCTGCCTTCATTGAGAACCTCCGGCGGCGGTTCCGGGAGAACCTCATTTATACCTAC 205
                                                                                                                                                                                                       206 ATCGGTCCTGTCCTAGTCTCTGTCAATCCCTACCGAGACCTACAGATCTACAGCCGGCAG 265
                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: CH 0016/97 FILING DATE: 31-DEC-1996
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                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Meigs, J. Timothy REGISTRATION NUMBER: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                 GCGGAGCAGGCATACCGCAACTTGTTGACACAGAGGCAGGACCAGTCGGTGTTAGTAACA 43
                                                                                                                                                                       TCTGGGCTATTCCTCGTCGCGTTGAATCCGTACAGCAACATCAAGGTGTACACGCAGGAC 163
                                                                                                                                                                                                                                         GAGGCGTCTGTGTACAACTTGGAGAACCGATACAAGGACGATATGATATACTTAT 223
                                                                  GCTGACACTGTATACCGGGCACTTCGTACTGAGCGTCGGGACCAGGCAGTGATGATTTCT 385
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No. 6239264th Carolina
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/ENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wendland, Jurgen
Knechtle, Philipp
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Steiner, Sabine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                           Score 80.2; DB 4; Pred. No. 2.8e-12;
                                                                                                                                                                                                                                                                                                             Mismatches 123;
                                                                                                                                                                                                                                                                                                                                           Length 693;
                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                          ; IDENTIFICATION METHOD: Von Heijne matrix; OTHER INFORMATION: SCORE 3.6; OTHER INFORMATION: Seq CTSLLQLYDASNS/EW US-08-905-223-162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 4
US-08-905-223-162
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Sequence 162, App...
No. 6222029
                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO:
                                                                                                                                                          1858 GCCAAGCAGCCGGGTCGCTTTGATGAGGTGCTCATCCGACATCAGGTGAAGTACCTGGGA 1917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Israelsen, Ned A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: STREET CITY: San Diego CTY: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                            1978 TTCCTGCAGAGGTACAAGTCACTG 2001
                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                            1918 CTGATGGAGAATCTGCGCGTGCGCAGAGCTGGCTTTGCCTATCGTCGCAAATATGAGGCT 1977
                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 29
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                                                                                                                                                                                                                                                                                                                        NAME/KEY: sig_peptide LOCATION: 56..271
                                                                                                                                                                                                                                                                                                                                                                   TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
TOPOLOGY: LII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy Disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 92101-3505
                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
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                                                                                                                            GGCTAGATGCCAGACCAGTTTGACCAGGCGGTTGTGCTGAACCAGCTGCGGTACTCAGGG 109
TTTTACAAAAGGTATAAAGTGCTG 193
                                                            ATGCTGGAGACTGTGAGAATCCGCAAAGCTGGGTATGCGGTCCGAAGACCCCTTTCAGGAC 169
                                                                                                                                                                                           81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEIC ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    364 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Edwards, Jean-Baptiste
Duelert, Aymeric
                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   SS: DOUBLE LINEAR
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PENTION: 5' ESTS FOR SECRETED PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                      Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Knobbe, Martens, Olson & Bear
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                                                                                                                                                                                                                                                                                                                                                                       Brain
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56.2%;
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                                                                                                                                                                                          Score 43.2; DB 4;
Pred. No. 0.029;
0; Mismatches 63;
                                                                                                                                                                                             63;
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                                                                                                                                                                                           Indels.
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RESULT 5

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RESULT 6
US-08-403-852D-4
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                 GENERAL INFORMATION:
APPLICANT: Blanc,
APPLICANT: Blanche
APPLICANT: Crouzet
                                                                                                                                              Sequence 4, Application US/08403852D Patent No. 5891695
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REFERENCE/DOCKET NUMBER: A544
TELECOMMUNICATION INFORMATION:
TELEFAX: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 343 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No.
                                                                                                                                                                                                                                                                                                                                                                           1387 CTTCAACAAGATCATCTGTGACCTGGTAGAGGAGAAGTT 1428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1267 CGAGCAGTTCTGCATCAACTGCAATGAGAAGCTGCAGCAGCTGCTTCATCGAGCTGAC 1326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Gicquel, ITITLE OF INVENTION: ITITLE OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/623,729
FILING DATE: 14-DEC-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                     259 GGTGGGCGACCAGTCGATCGGTGACCTGATCGCCGAGGCGAT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
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APPLICANT: Grandchamp-Desraux, Bernard
APPLICANT: Levy-Frebullt, Veronique
APPLICANT: Gicquel, Brigitte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Dreger, Walter H
REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 06-JUICLASSIFICATION: 435
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CITY: San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCTCAAGTCGGAGCAGGAGGAATACGAGGCTGAGGGCATCGCGTGGGAACCTGTCCAGTA 1386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAACCTGCTCAGCTTCAAGTGCGGCATCGAGAAGGCGGTCGAGAAGGTCACCGAGACCCT 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCTCAAGCCGGCCAAGGAGGTCGAGACCAAGGAGCAGATCGCCGCGACCGCCGTGATCTC 258
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l Similarity 53.18;
86; Conservation
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5. 5877273
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                 Blanc, Veronique
Blanche, Francis
Crouzet, Joel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-JUN-1995
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US-08-403-852D-4
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INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1208 bass ---
Type:
                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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APPLICATION NUMBER: FR 92,
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISSTRATION NUMBER: 25, 14
REFERENCE/DOCKET NUMBER: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Debussche, La
APPLICANT: De Crecy-Laga
TITLE OF INVENTION: Poly
TITLE OF INVENTION: Bios
TITLE OF INVENTION: Codi
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
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NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE NYPOTHETICAL: N
                                    747
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                                                                     467
                                                                                                     687
                                                                                                                                      407
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: PCT/
FILING DATE: 25-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/01
FILING DATE: 10-MAY-1995
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AGACCCAGGTCACCAT 542
                                 ACCCCCAGAGCTACTT 762
                                                           CGCGCCGGCTCACCGAGGTCCGCAAGGACGGCACCGTCCCCTACCTGCGCCCCGACGGCA
                                                                                       TTTACCAGCTACTGGAGGGGGGGGAGGAGGACTCTCCGTCGGCTGGGCTTGGAACGGA 746
                                                                                                                                                         ACCTCCTGGAAAAGTCCCGGGTGGTGCACCAAAATCACGGAGAGCGGAACTTCCACGTCT 686
                                                                                                                                                                                        AGGGCGAGGACGAGCTCGACCAGCAGGGGCGCGGCGACCAGGGCCTGATGTTCGGCT 406
                                                                                                                                                                                                                          AGTACATGGATGTGCAGTTTGACTTCAAGGGTGCCCCCGTGGGAGGCCACATTCTCAGTT 626
                                                                                                                          ACGCCACCGACGAGACCCCCTCGCTGATGCCGCTGCCCATCGAGCTCGCCCACCGCCTCT
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                                                                                                                                                                                                                                                                  Conservative
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1..1208
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VENTION: Polypeptides Involved In The
VENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
VENTION: Coding For These Polypeptides And Their Use
EQUENCES: 43
                                                                                                                                                                                                                                                                                                                                                                                                 S.pristinaespiralis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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Lacroix, Patricia
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                                                                                                                                                                                                                                                              Score 39.2; DB Pred. No. 0.68; 0; Mismatches
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; LOCATION:
US-08-510-646B-4
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Query Match
Best Local Similarity 50.v
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                              NFORMATION FOR SEQ ID NO:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FR 9
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR 93/00923
FILING DATE: 25-SEP-1993
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                         FEATURE:
NAME/KEY:
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                                                                                                                                                      ORIGINAL SOURCE:
                                                                                                                                                                                  MOLECULE TYPE: CD
                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1208 base pairs
                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                     HYPOTHETICAL:
ANTI-SENSE: NO
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OPERATING SYSTEM:
SOFTWARE: PatentI
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                                                                                                                                                                                                                                                                                                                                                        NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806.0054-01000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
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                                                                                                                                      ORGANISM:
                                                                                                                                                                                                                               STRANDEDNESS:
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                                                                                                                                                                                                                                             nucleic acid
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VENTION: Polypeptides Involved In The
VENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
VENTION: Coding For These Polypeptides And Their Use
EQUENCES: 45
                                                                                                                                                                                                                                                                                                                (202)
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                                                                                       1..1208
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                             (202) 408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-AUG-1995
                                                                                                                                                                                                     CDNA
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25-SEP-1992
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                                                                                                                                                                                                                                                                                                            408-4400
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                                                                                                                                                                                                                                                                                                4.
              0;
                           Score 39.2; DB 3; Length 1208; Pred. No. 0.68;
              Mismatches
              98;
            Indels
              0,
           Gaps
              0;
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567 AGTACATGGATGTGCAGTTTGACTTCAAGGGTGCCCCCGTGGGAGGCCACATTCTCAGTT 626

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US-09-231-818-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL
                                                                                                                        TELEFAX: (202) 408-44 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                          NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                    FILING DATE: 25-SEP-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
MOLECULE TYPE:
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
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                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/UN APPLICATION NUMBER: US/UN APPLICATION DATE: 10-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE:
                                                   TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 25-SEF
                                 TOPOLOGY:
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                                                                                     LENGTH:
                                                                                                                                                           TELEPHONE:
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20005-3315
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1300 I Street, N.W., Suite 700
                                                                                   1208 base pairs
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Debussche, Laurent
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                                 linear
                                                                                                                                                           (202) 408-4000
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25-SEP-1992
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                                                                                                                                           408-4400
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Biosynthesis Of Streptogramins, Nucleotide Sequences
Coding For These Polypeptides And Their Use
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US-08-403-852D-1
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Best Local Similarity
Watches 98; Conserve
                                                 TELECOMMUNICATION INFORMATION:
                                                                                                       APPLICATION UNBER: FR 92/11441
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 5891695
                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/08/403,0020
APPLICATION NUMBER: US/08/403,0020
FILING DATE: 10-MAY 1995
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: PCT/FR 93/00923
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DC SOFTWARE: Patentin Rela
                                                      NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806.0054-00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Debussche, Laurent
APPLICANT: De Crecy-Lagard, Valerie
TITLE OF INVENTION: Polypeptides Involved In The
TITLE OF INVENTION: Blosynthesis Of Streptogramins, Nucleotide Sequences
TITLE OF INVENTION: Coding For These Polypeptides And Their Use
                                             TELEPHONE:
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APPLICANT:
APPLICANT:
APPLICANT:
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CITY: Washington
STATE: D.C.
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ORGANISM: S.pristinaespiralis
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Crouzet, Joel
Jacques, Nathalie
Lacroix, Patricia
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Zagorec, Monique
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Pred. No. 0.68;
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                                                                   COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PATCHILL PROS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/510,646B
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US-08-510-646B-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
      PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/403,852
FILING DATE: 10-MAY-1995
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                 APPLICANT: Debussche, Laurent
APPLICANT: Decry-Lagard, Valerie
TITLE OF INVENTION: Polypeptides Involved In The
TITLE OF INVENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 532 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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APPLICANT:
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APPLICANT:
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CITY: Washington
STATE: D.C.
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HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: S.pr:
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Zagorec, Monique
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Crouzet, Joel
Jacques, Nathalie
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50.0%; Pred. No. 1
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Mismatches

DB 2;

Length 5392; Indels

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PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/ FILING DATE: 25-SEP-1993

PCT/FR 93/00923

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Patent No. 6171846
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TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5392 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                      TITLE OF INVENTION: ITITLE OF INVENTION: ITITLE OF INVENTION: OF SEQUENCES:
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REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 031
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4084 AGACCCAGGTCACCAT 4099
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HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                          APPLICANT:
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Local Similarity 50.0%;
hes 98; Conservative
                                     COUNTRY: USA
ZIP: 20005-3315
                                                                            STATE:
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STRANDEDNESS: doub
                                                                                           CITY: Washington
                                                                                                                 STREET:
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                                                                            D.C
                                                                                                             E: Finnegan, Henderson, Farabow, Garrett & Dunner 1300 I Street, N.W., Suite 700
                                                                                                                                                                            Dedussing, Tagard, Valerie

De Crecy-Lagard, Valerie

NENTION: Polypeptides Involved In The

NENTION: Biosynthesis Of Streptogramins, Nucleotide Sequences

NENTION: Polypeptides And Their Use
                                                                                                                                                                                                                                                                  Debussche, Laurent
                                                                                                                                                                                                                                                                                       Zagorec, Monique
                                                                                                                                                                                                                                                                                                     Thibaut, Denis
                                                                                                                                                                                                                                                                                                                          Lacroix, Patricia
                                                                                                                                                                                                                                                                                                                                          Jacques, Nathalie
                                                                                                                                                                                                                                                                                                                                                                Crouzet, Joel
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                                                                                                                                                                        Coding For These Polypeptides And 43
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Pred. No. 1.5;
0; Mismatches 98; Indels 0
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US-09-103-840A-1/c
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                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: FIEISCHAAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
                SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 1
                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09103840A Patent No. 6294328
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                                                     APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRATITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FR 92/11441
FILING DATE: 25-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03806.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (202) 408-44
INFORMATION FOR SEQ ID NO:
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ORIGINAL SOURCE:
ORGANISM: S.pr
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MOLECULE TYPE: CDN
MOLECULE TYPE: NO
LENGTH: 4411529
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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Local Similarity 50.08;
hes 98; Conserva+:...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCTCCTGGAAAAGTCCCGGGTGGTGCACCAAAATCACGGAGAGCGGAACTTCCACGTCT 686
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TIMBER: PCT/FR 93/00923
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ID NO: 1:
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Pred. No. 1.5;
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RESULT 14
US-08-471-033-24
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LOCATION: 1105
OTHER INFORMATION: unknown
US-09-339-993-1
                                                                                          Sequence 24, Application US/08471033 Patent No. 5770696
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US-09-339-993-1
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                                             GENERAL INFORMATION:
APPLICANT: Warren,
APPLICANT: Koziel
                                                                                                                                                                                                                                                                                                                                                                        Query Match 1.1
Best Local Similarity 53.6
Matches 81; Conservative
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; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37RV
US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 47
SEQ ID NO 1
LENGTH: 1664
TYPE: DNA
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APPLICANT: Lex M. C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09339993A Patent No. 6040179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: LEX M. COWSETE
TITLE OF INVENTION: ANTISENSE MODULATION OF G-ALPHA-12 EXPRESSION
FILE REFERENCE: RTS-0064
CURRENT APPLICATION NUMBER: US/09/339,993A
CURRENT FILING DATE: 1999-06-25
   APPLICANT:
APPLICANT:
APPLICANT:
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LOCATION: (78)..(1145)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1368 CGTGGGAACCTGTCCAGTACTTCAACAACAACATCATCTGTGACCTGGTAGAGGAGGAAGT 1427
                                                                                                                                                                               329 TGTCAAAGCCATGGGCAACCTGCAGATCGAC 359
                                                                                                                                                                                                   226 TGTCAATCCCTACCGAGACCTACAGATCTAC 256
                                                                                                                                                                                                                                    269 GGAATGCCGGCAGTACCGGGCGGTTGTCTACAGCAACACCATCCAGTCCATCATGGCCAT 328
                                                                                                                                                                                                                                                        166 CCTCCGGCGGCGGTTCCCGGGAGACCTCATTTATACCTACATCGGTCCTGTCCCTAGTCTC 225
                                                                                                                                                                                                                                                                                                                    106 AGGGGTGCAGGACTTTGTCCTGCTGGAGAATTTCACCAGTGAGGCTGCCTTCATTGAGAA 165
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nes 83; Conserv
                                                                                                                                                                                                                                                                                                AGGAAGAGCACCATCGTCAAGCAGATGAAGATCATCCACGAGGATGGCTACTCCGAGGA 268
                          Warren, Gregory W
Koziel, Michael G
Mullins, Martha A
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illarity 53.2%;
Conservative
, Gordon J
c, Brian
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Pred. No. 0.91;
0; Mismatches 7
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Pred. No. 32;
                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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Best Local Similarity 45.3
174; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                  1430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PILING DATE: 09-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/
FILING DATE: 23-MAR-1994
PRIOR APPLICATION DATA:
                                                                                                                     1310 CTCTTCATCGAGCTGACTCTCAAGTCGGAGCAGGAGGAATACGAGGCTGAGGGCATCGCG 1369
                                                                                                                                                                                   1250 TITCAGCATAACAGCTTCGAGCAGTTCTGCATCAACTACTGCAATGAGAAGCTGCAGCAG 1309
                                                                                                                                                                                                                                                          1190 AGCCCCAGCTGGCGAAGCACCACGGTTCTTGGGCTCCTGGACATTTACGGCTTTGAAGTG 1249
                                265 ACCGAGAAGGCCAAGATGAACAACTTCCTGGACAACAAGAACGACGACATCAAGACCAACTAC 324
                                                                                              205 GACAAGGAGAAGGCCAAGGAGTGGGGGCAAGGAAGGAGAAGGAGTGGAAGCTTACCGCC 264
                                                                                                                                                                                145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Pace, Gary M.
REGISTRATION NUMBER: P-40,4
REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION INFORMATION:
TELECHONE: 919-541-8582
                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/037,057
FILING DATE: 25-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Desal, National Applicant: Kostichka, N. Kristy
APPLICANT: Kostichka, N. Kristy
APPLICANT: Duck, Nicholas B
APPLICANT: Estruch, Juan J
TITLE OF INVENTION: No. 5770696el Pesticidal Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature LOCATION: 1..1386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 1399 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 919-541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: Patenti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
AAGGGCATCATCTCCATCTTGGATGAAGAGTGCCTGCGTCCTGGGGGAGGCCACGGACCTG 1489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 7 Skylin
CITY: Hawthorne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
                                                              TGGGAACCTGTCCAGTACTTCAACAACAAGATCATCTGTGACCTGGTAGAGGAGAAGTTC 1429
                                                                                                                                                              AGCAAGTACACCAACCTCCAGAACCTGAAGATCACCGACAAGGTGGAGGACTTCAAGGAG
                                                                                                                                                                                                                            AGCATCAGCCTGCTGAACAACGAGGTGATCAAGGCCGAGCAGCTGAACATCAACAGCCAG
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA
                                                                                                                                                                                                                                                                                                                   1.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (genomic)
                                                                                                                                                                                                                                                                                                                                                                          /note= "Maize optimized DNA
sequence for VIP2A(a) protein from
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Pred. No. 1.1;
0; Mismatches 199; Indels 6
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US-08-471-044-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 24,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                       TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: APPLICANT:
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                                                                                                                                                                                     NAME: PACE, GATY M.
REGISTRATION NUMBER: 40,403
REFERENCE/DOCKET NUMBER: CG(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Estruch, Juan J
TITLE OF INVENTION: NO. 5840868el Pesticidal Proteins and Strains
NUMBER OF SEQUENCE: 50
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1490
                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 05-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/314,594
FILING DATE: 09-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/463,483
FILING DATE: 05-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
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                                    FEATURE:
                                                   MOLECULE TYPE:
                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: / CONTROL Hawthorne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: UZIP: 10532
LOCATION:
                  NAME/KEY:
                                                                   TOPOLOGY:
                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                    FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: CIBA-GEIGY Corporation STREET: 7 Skyline Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AACGTGGAGCCCACCACCA 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCTTTCTGGAGAAGTTGGAGGACACTGTCAAGCCCCACCCTCACTTCCTGACGCACAAG 1549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGGAGATCGACAAGATGTTCGACAAGACCAACCTGAGCAACAGCATCATCACCTACAAG 438
                                                                                                nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Warren, Gregory W
Koziel, Michael G
Mullins, Martha A
Nye, Gordon J
                                                                                                                   1399 base pairs
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misc_feature
1..1386
                                                                                                                                                                                                                                                                                                  NUMBER: US 08/037,057
25-MAR-1993
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                                                 DNA (genomic)
                                                                                  single
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                                                                                                                                                         24:
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; OTHER INFORMATION: ; OTHER INFORMATION: US-08-471-044-24 Qy οy δÃ DЬ Qy В δõ В δÃ В QΥ B 밁 Search completed: December Job time: 12768 secs 1.18; best Local Similarity 45.98; Matches 174; Conservative 1490 1430 AAGGGCATCATCTCCATCTTGGATGAAGAGTGCCTGCGTCCTGGGGAGGCCACGGACCTG 1489 1370 1310 CTCTTCATCGAGCTGACTCTCAAGTCGGAGCAGGAGGAATACGAGGCTGAGGGCATCGCG 1369 1190 AGCCCCAGCTGGCGAAGCACCACGGTTCTTGGGCCTCCTGGACATTTACGGCTTTGAAGTG 1249 1250 TTTCAGCATAACAGCTTCGAGCAGTTCTGCATCAACTACTGCAATGAGAAGCTGCAGCAG 1309 439 379 325 205 145 265 ACCGAGAAGGGCAAGATGAACAACTTCCTGGACAACAAGAACGACATCAAGACCAACTAC 85 CTCGCTGACCAGAAGACCA 1568 TGGGAACCTGTCCAGTACTTCAACAACAAGATCATCTGTGACCTGGTAGAGGAGGAGAAGTTC 1429 AAGGAGATCACCTTCAGCATGGCCGGCAGCTTCGAG-----GACGAGATCAAGGACCTG AGCAAGTACACCAACCTCCAGAACCTGAAGATCACCGACAAGGTGGAGGACTTCAAGGAG 204 AGCATCAGCCTGCTGAACAACGAGGTGATCAAGGCCGAGCAGCTGAACATCAACAGCCAG 144 AACGTGGAGCCCACCACCA 457 ACCTTTCTGGAGAAGTTGGAGGACACTGTCAAGCCCCACCCTCACTTCCTGACGCACAAG 1549 AAGGAGATCGACAAGATGTTCGACAAGACCAACCTGAGCAACAGCATCATCACCTACAAG /note= "Maize optimized DNA
sequence for VIP2A(a) protein from AB78" 9 2002, 18:43:28 0, Score 38.6; DI Pred. No. 1.1; Mismatches DB 2; 199; Length 1399; Indels 6 Gaps 324 378 ۳.

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Maximum
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Title:
Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                       score greater than or equal to the score of the result beir and is derived by analysis of the total score distribution
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Gapop 10.0 , Gapext 1.0
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3661
                                                                                                                                                                                                                                                                                                                             Match Length
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                                                                                                                                                                                                                                                                                                                                            Query
     Published_Applications_NA: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq *
/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq *
/cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq *
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Copyright (c) 1993 - 2002 Compugen Ltd
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/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
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                0 US-09-880-107-3357
0 US-09-925-300-643
2 US-10-044-090-588
0 US-09-954-456-2215
0 US-09-954-445-726
0 US-09-938-842A-977
0 US-09-925-302-243
0 US-09-925-302-243
0 US-09-925-302-243
0 US-09-9834-975-1025
0 US-09-851-682A-2
0 US-09-851-78-945
0 US-09-815-343-787
0 US-09-815-343-787
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Sequence 3357, Apsequence 543, App Sequence 588, App Sequence 2215, Ap Sequence 726, App Sequence 777, App Sequence 171, App Sequence 1025, Ap Sequence 1025, Ap Sequence 1025, Ap Sequence 340, App Sequence 945, App Sequence 945, App Sequence 638, App Sequence 64, App Sequence 79, Appl Sequence 79, Appl Sequence 79, Appl Sequence 2116, Appl Sequence 2116, Appl
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40.2	40.6	41.6	43	43	43.2	43.8	43.8	45.4	45.4	45.4	45.6	50.2	52.2	52.2	52.2	52.8	58.8	60.4	61.6	63.4	63.4	65.6	66.4	70.2	71.6
1.1	1.1	1.1	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.2	1.4	1.4	1.4	1.4	1.4	1.6	1.6	1.7	1.7	1.7	1.8	1.8	1.9	2.0
3951	1702	2451	311	311	302	4701	578	479	307	175	568	90	8117	7707	2953	583	491	87	432	590	233	30013	574	188	558
	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10
US-09-712-363-31	US-09-880-107-3680	US-09-815-242-9849	US-09-864-761-25016	US-09-864-761-17687	US-09-864-761-23022	US-09-864-864-326	US-09-864-761-8283	US-09-864-761-5359	US-09-864-761-24840	US-09-864-761-22133	US-09-864-761-8095	US-09-864-761-25597	US-09-866-108-1	US-09-866-108-2	US-09-866-108-4	US-09-864-761-8935	US-09-728-446-1370	US-09-864-761-31392	US-09-960-352-12994	US-09-864-761-15884	US-09-864-761-32388	US-09-764-877-3297	US-09-864-761-14865	US-09-864-761-23611	US-09-864-761-6878
Sequence 31, Appl	Sequence 3680, Ap	Sequence 9849, Ap	Sequence 25016, A	Sequence 17687, A	Sequence 23022, A	Sequence 326, App	Sequence 8283, Ap	Sequence 5359, Ap		Sequence 22133, A	Sequence 8095, Ap	25	Sequence 1, Appli	Sequence 2, Appli	4, App	8935,	Sequence 1370, Ap	Sequence 31392, A	Sequence 12994, A	Sequence 15884, A	Sequence 32388, A	Sequence 3297, Ap	Sequence 14865, A	Sequence 23611, A	Sequence 6878, Ap

## ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver. 2.1
SEO ID NO 3357
LENGTH: 7465
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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: Sequence 3357, Application US/09880107

: Patent No. US20020142981A1

: GENERAL INFORMATION:
                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 1129; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer FILE REFERENCE: 44921-5028-WO CURRENT APPLICATION NUMBER: US/09/880,107 CURRENT FILING DATE: 2001-06-14 PRIOR APPLICATION NUMBER: US 60/211,379 PRIOR TILING DATE: 2000-06-14 PRIOR PRIOR DATE: 2000-06-14 PRIOR PRIOR DATE: 2000-06-14 PRIOR PRIOR DATE: 2000-10-02 NUMBER: US 60/237,054 PRIOR FILING DATE: 2000-10-02 NUMBER: OS 60/237,054 PRIOR FILING DATE: 2000-10-02 NUMBER: OS 500 ID NOS: 3950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Joseph (
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
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585 GTGAACCCCTACCAGCTGCTCCCATCTACTCGCCAGAGCACATCCGCCAGTATACCAAC
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                            GTCAATCCCTACCGAGACCTACAGATCTACAGCCGGCAGCATATGGAACGCTACCGTGGT
                                                                                                               CTCCGGCGGTTCCGGGAGAACCTCATTTATACCTACATCGGTCCTGTCCTAGTCTCT 226
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CACCTGCAGCAGTTCTTTGTGCGGCACGTGTTCAAGCTGGAGCAGGAGGAATATGACCTG
                  AAGCTGCAGCAGCTCTTCATCGAGCTGACTCTCAAGTCGGAGCAGGAGGAATACGAGCCT
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GCTGCCACACTGATCCAGAGGCACTGGCGGGGTCACAACTGTAGGAAGAA
                           TCAGCCATCTGTATCCAGTCATGGTGGCGTGGCACACTGGGCCGGAGGAA
                                                    CTCCTTCAGAAAGTCATCCGGGGATTCAAAGACAGGTCTAACTTTCTGAAGCTGAAGAAC
                                                                                                            CACCATGACATGCTGCTGGAAGTGGAGCGGGACAAAGCCCATCACCGACAG---AGTCATC
                                                                              AAGATCCAGGCGGCCTGGAGGGGCTTTCATTGGCGACAGAAATTTCTCCGGGTGAAGCGA
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RESULT 2
US-09-925-300-643
/ Sequence 643, Application US/09
/ Patent No. US20020151881A1
/ GENERAL IMPORMATION:
/ APPLICANT: Craig Rosen,
/ APPLICANT: Steve Ruben
/ TITLE OF INVENTION: Nucleic Ac US/09925300

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Acids, Proteins and Antibodies

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: FEATURE:
: NAME/KEY: misc feature
: LOCATION: (8)
: OTHER INFORMATION: n equals a,
: NAME/KEY: misc feature
: LOCATION: (1664)
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CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
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SEQ ID NO 643
LENGTH: 1712
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Best Local Similarity
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AGCCATGCCCTCATCAAGTCTTTGTTCCCCGGAAGGGAATCCCGCCAAGATCAACCTGAAA
                                   ATGAACCCCATCATGGCCCAGTGCTTTGACAAGAGTGAGCTCAGTGACAAGAAGCGGCCA 1759
                                                                         TTCGTTGACAAAAACAATGACCTTMTCTATCGAGACCTGTCCCAAGCCATGTGGAAGGCC
                                                                                               TTTCTGGATAAAAACAATGACCTCCTCTTCCGGAACCTGAAGGAGACCATGTGCAGCTCA
                                                                                                                                                    CCTCACAGCTGCTTCAGGATCCAGCATTATGCTGGAAAGGTGCTGTACCAGGTGGAAGGA
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Pred. No. 1.1e-77;
Pred. Mismatches 510;
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APPLICANT: Olga Bandman
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN
FILE REFERENCE: PA-0028 US
CURRENT APPLICATION NUMBER: US/10/044,090
CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL Program
SEQ ID NO 588
LENGTH: 3632
TYPE: DNA
ORGANISM: Homo sapiens
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; OTHER INFORMATION: Incyte ID
US-10-044-090-588
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Best Local Similarity
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                                                       TTTGAGCAGTTCATTATTAATTATTGTAACGAAAAGCTGCAACAAATCTTCATTGAACTT 243
                                                                                             TTCGAGCAGTTCTGCATCAACTACTGCAATGAGAAGCTGCAGCAGCTCTTCATCGAGCTG 1324
                                                                                                                                   AGAAAGAAGGTCATGGGTGTTCTGGACATTTATGGCTTTGAGATTTTCGAGGACAACAGC 183
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Sequence 2215. Application US/09954456

Patent No. US20020115057A1

GENERAL INFORMATION:
APPLICANT: YOUNG, Paul
TITLE OF INVENTION: Process for Identifying
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-76

CURRENT APPLICATION NUMBER: US/09/954,456
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US-09-954-456-2215
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PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR FILING DATE: 2000-09-26
PRIOR FILING DATE: 2000-09-25
PRIOR PRIOR TILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR APPLICATION NUMBER: US/60/235,638
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,711
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,711
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,720
PRIOR APPLICATION NUMBER: US/60/235,720
PRIOR APPLICATION NUMBER: US/60/235,840
PRIOR FILING DATE: 2000-09-27
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 2215
LENGTH: 7596
TYPE: NO.
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Best Local Similarity
Matches 647; Conserv
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 898 TCAAGCAAAAGATGAACGTACTTTTCATATCTTTTACCAGTTGTT--ATCTGGAGCAGGA
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                   TGTGAAAAATGATAACTCATCTCGTTTTTGGCAAATTTATTCGGATCAACTTTGATGTAAC
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                                                      US-10-044-303-3
                                                                                                                                                  TITLE OF INVENTION: Protein expression and structure TITLE OF INVENTION: specific fusion vectors FILE REFERENCE: ST010209-EPA CURRENT APPLICATION NUMBER: US/10/044,303 CURRENT FILING DATE: 2002-01-11 NUMBER OF SEQ ID NOS: 3 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 3 LENGTH: 3048
                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Max-Planck-Gesellschaft e.V.
                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/10044303 Patent No. US20020137161A1
Query Match
Best Local Similarity
                                                             ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: DNA
OTHER INFORMATION: coding for recombinant protein M761-2R F
                                                                                                                                          TYPE: DNA
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                                                   GAACCACGTATTTTAGCCGGTCGTGATTTAGTTGCTCAACATCTCAACGTTGAAAAATCC
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                                                                                                                                                                                                                                                                   GGTTTCTCACAAGAAGAACAAATGTCAATCTTTAAGATCATTGCTGGTATCTTACATTTA 1074
                                                                                                                                                                                                                                                                                                                       ATCAAAGGTGTCTCTGATAGTGAAGAATTCAAAATCACTCGTCAAGCTATGGACATTGTT 1014
                                                                                                                                                                                                                                                                                                                                                                          CTTCACTTGGCTGGT---CCAGAATCATTCAACTACTTAAATCAAAGTGGTTGTTGAT 954
                                                                                                                                                           CTCAACGCTGCTTCAACCGTCTTTGGTGTCAATCCATCAGTCCTTGAAAAGGCTCTCATG
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APPLICANT: Zambrowicz, Brian
APPLICANT: Zambrowicz, Brian
APPLICANT: Sands, Arthur T.
APPLICANT: Sands, Arthur T.
TITLE OF INVENTION: NO. US20020102543A1e1 Mutated Mammalian Cells and TITLE OF INVENTION: No. IS20020102543A1e1 Mutated Mammalian Cells and CURENT APPLICATION NUMBER: US/09/728,445
CURRENT APPLICATION NUMBER: US/09/728,445
CURRENT APPLICATION NUMBER: US 60/168,358
PRIOR APPLICATION NUMBER: US 60/168,358
PRIOR FILING DATE: 1999-12-01
NUMBER OF SEQ ID NOS: 891
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 457
TYPE: DNA
DDCANTEN: Miss missouling
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: OTHER INFORMATION: n = A,T,C or US-09-728-445-726
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Best Local
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Patent No. US20020102543A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
       361
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                                                                 343 GGCACTTCGTACTGAGC--GTCGGGACCAGGCAGTGATTT-----CTGGAGAGAGTG
                                                                                                     241 NNAGTANNNTANGACNGTNCCANCCTCATTTNGTTNGCACNGGCTTGACACTGTATACCG
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                         GGGCAGGCAAGACAGAGGCCACCAAGA 422
                                               GGCACTTCGTACTGAGCAGTCGAGNACCCGGCAGTGATGATTNTCTGGGNNGAGAGCGGG
                                                                                                                                                                                                                 GGCAAGGCAAGACAGAGACACAAGA
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                                                                                                                        TTTCTATGAAGTACCACCTC-----ATTTGTTTGCAGTGGG-TGACACTGTATACCG
                                                                                                                                                           TCCCTACCGAGACCTACAGATCTACNGCCCGGCATCTTATTTNAACGGGNNNCGTGNTAG
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73.98;
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Pred. No. 2.4e-41;
0; Mismatches 83;
387
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PRIOR FILING DATE: 2001-06-22

NUMBER OF SEQ ID NOS: 5379

SEQ ID NO 97

LENGTH: 3501

TYPE: DNA

OGGANISM: Arabidopsis thaliana
US-09-938-842A-977
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APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
APPLICANT: Joh, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLF
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLF
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE OF INVENTION: SOME, AND METHODS OF USE
CURRENT APPLICATION NUMBER: US/09/938,842A
PRIOR APPLICATION NUMBER: US/09/938,842A
PRIOR APPLICATION NUMBER: US 60/227,866
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
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US-09-938-842A-977
, Sequence 977, Application US/09938842A
, Patent No. US20020160378A1
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Best Local Similarity 48.6%;
Matches 656; Conservative
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                                      1023 ATGTGCTGAAGGGGAAAGGTCATATCATATTTTTATCAACTTTGTGCTGGGGCTTCACC
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GGAGACTCTCCGTCGGCTGGGCTTGGAACGGAACCCCCAGAGCTACTTGTACCTGGTGAA 774
                                                                                                                 TGGAAAGATATCGGGTGCTCAAATTCAAACCTTTTTACTAGAAAAGTCTAGAGTGGTCCA
                                                                                                                                                    GGGTGCCCCCGTGGGAGGCCACATTCTCAGTTACCTCCTGGAAAAGTCCCGGGTGGTGCA
                                                                                                                                                                                             ATTGAGAAATGATAATTCTAGTCGTTTTGGGAAGCTAATAGAGATTCATTTTAGTGAAAG
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                                                                                                                                                                                                                                                                        GATCGAATATGAGATACTTAAGACTAATCCCATTTTGGAAGCATTTGGAAATGCAAAAAC
                                                                 AGTGCGAGACCGCCTGTTTGCAGAGCAACCCCGTGTTAGAGGCCTTTTGGGAATGCCAAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                            CGATGAAGTTAACCAATCTATCATTATCAGCGGCGAGAGTGGAGCAGGGAAAACTGAGAC
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CURRENT APPLICATION NUMBER: US/09/925,302
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05918
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 896
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 243
FENCTH: 736
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                                                                                                                                                                                                                                                                                                                Sequence 243, Application US/09925302 Patent No. US20020044941A1
                                                                                                                                                                                                                                     APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins
FILE REFERENCE: PA104
ORGANISM: Homo sapiens FEATURE:
                                    TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GACAAGGGTTGATTTTGAGGACAACCAAAATTGTCTGAGTCTTTTTGAAAAAGAAACCATT 1784
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US-09-764-853-131; Sequence 131, Application US/09764853; Patent No. US20020090672A1
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US-09-764-853-131
                                                Prior application data removed - NUMBER OF SEO ID NOS: 939
SOFTWARE: PatentIn Ver. 2.0
SEO ID NO 131
LENGTH: 2339
                                                                                                                                                                          APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins,
FILE REFERENCE: PJZ06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/764,853
CURRENT FILING DATE: 2001-01-17
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OTHER INFORMATION: n e
              TYPE: DNA
ORGANISM: Homo sapiens
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Sequence 1025, Application US/09834975
Patent No. US20020110815A1
GENERAL INFORMATION:
APPLICANT: Lillie, James
APPLICANT: Botwn, Jeffrey
APPLICANT: Botk, Andrew
APPLICANT: Botk, Andrew
APPLICANT: Wall Huffel, Christophe
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS AND METHODS
TITLE OF INVENTION: FOR THE IDENTIFICATION, ASSESSMENT, PREVENTION,
TITLE OF INVENTION: OF HUMAN CANCERS
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Pred. No. 3e-30;
0; Mismatches 388;
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CURRENT APPLICATION NUMBER: US/09/834,975
CURRENT FILING DATE: 2001-04-13
PRIOR APPLICATION NUMBER: 60/197,538
PRIOR FILING DATE: 2000-04-14
NUMBER OF SEQ ID NOS: 1046
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 1025
LENGTH: 2345
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; LOCATION: (1)...(2345)
; OTHER INFORMATION: n = A,T,C
US-09-834-975-1025
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Best Local
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                                                         ATCAACTACACCAATGAGAAGCTGCAGCAGCTGTTCAACCACCATGTTTATCCTAGAA
               ATCAACTACTGCAATGAGAAGCTGCAGCAGCTCTTCATCGAGCTGACTCTCAAGTCGGAG
                                                                                                                           AATAAAGCTCTG----
                                                                                                                                      AATAGGTCACTGGCCTCTAAGGACGCTGAGAGCCCCAGGTTGGCGAAGCACCACGGTTCTT
                                                                                                                                                                           GTAGAAGCATTGGCAAAAGCTACCTATGAGCGGCTCTTTCGCTGGCTCGTTCATCGCATC
                                                                                                                                                                                                                                                      ATCATCGCCAAGGGGAAGAGCTCCTGAGCCCACTGAACCTTGAACAGGCGGCATATGCA 1099
                                                                                                                                                                                                                                                                                                                                                                                                                                   GATGAAGTGGAGGACTTGCTCAGCATCGTGGCCAGCGTCCTACATCTGGGCAACATCCAC
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Pred. No. 8.8e-24;
0; Mismatches 382;
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TITLE OF INVENTION: MYOSIN IXA AND CYCLIC NUCLEOTIDE GATED TITLE OF INVENTION: CHANNEL-15 (CNGC-15) POLYNUCLEOTIDES, POLYN TITLE OF INVENTION: COMPOSITIONS, METHODS, AND USES THEREOF FILE REFERENCE: 200130.442

CURRENT APPLICATION NUMBER: US/09/851,682A

CURRENT FILING DATE: 2001-05-08

PRIOR APPLICATION NUMBER: US/09/172,422

PRIOR FILING DATE: 1998-10-14

NUMBER OF SEQ ID NOS: 3

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 2

LENCTH: 8473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 288;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   143 AGTGAGGCTGCCTTCATTGAGAACCTCCGGCGGCGGTTCCGGGAGAACCTCATTTATACC 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  714 AATGAGAAAACTCTCTTAGAAAACCTACGAGATCGCTTTAAGCATGAAAAAATTTATACC 773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                       GCTCTCAGTCAGAA----AGGATTTGCCAGTGGAGTAGAACAGATTATTCTTGGAGCTGGA 1070
                                                                                                                                                                                CCCGTGTTAGAGGCCTTTGGGAATGCCAAGACTCTCCGCAACGATAACTCCAGCCGGTTT 562
                                                                                                                                                                                                                                                                                                                                                                                              GTGGCTGACACTGTATACCGGGCACTTCGTACTGAGCGTCGGGACCAGGCAGTGATGATT 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGAAAGTACATGGATGTGCAGTTTGACTTCAAGGGTGCCCCCGTGGGAGGCCACATTCTC
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AAATATCTACTGGAGAAGTCCAGACTCGTTTATCAGGAGCATAATGAACGGAACTATCAT 1250
                                 AGTTACCTCCTGGAAAAGTCCCGGGTGCTGCACCAAAATCACGGAGAGCGGAACTTCCAC
                                                                                                                                               CCAGTACTTGAGGCCTTTGGAAATGCAAAGACAGCTCATAATAACAATTCAAGTCGTTTT
                                                                                                                                                                                                                                                          GAGACCTGCCCAGCCCCTGAACGGGGTGGCGCAGTGCGAGACCGCCTGTTGCAGAGCAAC
                                                                                                                                                                                                                                                                                                                                  TCTGGAGAGAGTGGGGCAGGCAAGACAGAGGCCACCAAGAGACTGCTCCAGTTCTATGCA 442
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                                                                     GGGAAGTTTATTCAAGTAAATTACCAGGAAACAGGCACTGTACTTGGTGCCTATGTTGAA
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Sheffield, Val
Welch, Juliet
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Duhl, David
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Sequence 945, Application US/10046935

Patent No. US20020156011A1

GENERAL INFORMATION:
APPLICANT: Jiang, Yuqiu
APPLICANT: Harlocker, Susan L.
APPLICANT: Secrist, Heather
APPLICANT: Wang, Aijun
APPLICANT: Wang, Aijun
APPLICANT: Stolk, John A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
FILE REFERENCE: 210121.527C1
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US-09-764-853-340
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 340
LENGTH: 666
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Best Local Similarity
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OTHER INFORMATION: n e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and
FILE REFERENCE: PJZ06
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CURRENT FILING DATE: 2001-01-17
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NAME/KEY: SITE
LOCATION: (181)
CURRENT APPLICATION NUMBER: US/10/046,935
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63.5%; Pred. No. 3.4¢
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Sequence 945. Application US/09878178
Patent No. US20020177552A1
GENERAL INFORMATION:
APPLICANT: Jiang, Yuqiu
APPLICANT: Harlocker, Susan L.
APPLICANT: Heather
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.527
CURRENT APPLICATION NUMBER: US/09/878,178
RUMBER OF SED ID NOS: 2237
SOUTMARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                            ; LENGTH: 360
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-878-178-945
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US-09-878-178-945
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; ORGANISM: Homo saplens
US-10-046-935-945
2030 GACGGCCCCAGGATGGTGTGGCCGTGTTGGTCAGACACCTTCGGCTACAAGCCAGAAGAGT
                                                                                                      1910 ACCTGGGACTGATGGAGAATCTGCGCGTGCGCTAGAGCTGGCTTTGCCTATCGTCGCAAAT 1969
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NUMBER OF SEQ ID NOS: 2239
SOFTWARE: FASTSEQ FOR Windows Version 4.0
SEQ ID NO 945
LENGTH: 360
muore: Num
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Best Local Similarity 55.6%;
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55.6%; Pred. No. 1.1e-17;
ative 0; Mismatches 147;
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Pred. No. 1.1e-17;
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NAME/KEY: misc_feature
LOCARTION: (1)...(476)
OTHER INFORMATION: n = A,T,C
US-09-815-343-787
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Best Local Similarity 54...
224; Conservative
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US-09-815-343-787
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CURRENT FILING DATE: 2001-03-22
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: FASTSEQ for Windows Version 4.0
LENGTH A. A. A.
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APPLICANT: Xu, Jiangchun
APPLICANT: Xi, Jiangchun
APPLICANT: King, Gordon E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY
FILE REFERENCE: 210121.504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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Pattent No. US20010055596A1
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TYPE: DNA
ORGANISM: Homo sapien
                 876 ACTTGCTCAGCATCGTGGCCAGCGTCCTACATCTGGGCAACATCCACTT
355 GCCTGCTGNGGGTCATCTCAGGGGTTCTTCANCTCGGCNACATCGTCTT 403
                                                                                                                                                                    756
                                                                                                                                                                           181 TCCTGTCTGGGGCTGGAGAGCACCTGAAGACCGATCTCCTGTTGGAGCCGTA---CAACA
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                                                                          ACTGGAAGGTTATGAGGAAGGCGCTGTCCGTCATTGACTTCACTGAGGATGAAGTGGAGG
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                                                       TGTTCCACGAGACCATGGAGGCCATGAGGATTATGGGCATCCCAGAAGAGGAGCAAATGG
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Pred. No. 8.
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3661
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Gapop 10.0 , Gapext 1.0
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## ALIGNMENTS

REFERENCE AUTHORS TITLE JOURNAL REFERENCE REFERENCE SOURCE KEYWORDS VERSION ACCESSION DEFINITION LOCUS JOURNAL MEDLINE PUBMED MEDLINE PUBMED TITLE ORGANISM AUTHORS Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999) Genome Res. 20499374 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new construction of the constr Mus musculus (strain:C57BL/6J) adult clone\_lib:RIKEN full-length enriched AK004743 5198 bp Mus musculus adult male lung cDNA, Eukaryota; Mammalia; Mus musculus AK004743.1 GI:12836146 HTC; CAP trapper. library, clone:1200013G06:myosin Ic, full insert sequence. 99279253 clone:1200013G06. 11042159 0349636 a; Metazoa; ; Eutheria; 10 (10), 1617-1630 (2000) Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus mRNA linear HTC 19-JA RIKEN full-length enriched male 1 mouse lung o cDNA to mRNA, A library HTC 19-JAN-2002 genes Mus.

AUTHORS

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S Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Nurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Saito, H., Saito, R., Sakai, C., Sakai, K., Sono, H., Sasaki, D., Sochriml, L., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamanaka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M., and
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            Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Stitute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
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COMMENT

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282 GTGGTGTCAGTTTCTATGAAGTACCACCTCATTTGTTTGCAGTGGCTGACACTGTATACC
                                                                                 265 TCTCTGTCAATCCCTACCGAGACCTACAGATCTACAGCCGGCAGCATATGGAACGCTACC
                                                                                                                                                                                                                                                                                                                           102 GGGTAGGGGTGCAGGACTTTGTĆCTGCTGGAGAATTTCACCAGTGAGGCTGCCTTCATTG 161
                                                                                                                                                                                                                                                                                                                                                                                                 85 CGGCCTTGGGCAGTGACGGGTTCGAGTGACCATGGAGAGCGCCTTGACTGCCCGAGACC 144
                                                                                                                                                                                                                                                                                                                                                                                                                                   42 CGGCCCTGGGCAGTGACGGGGTTCGAGTGACCATGGAGAGCGCCTTGACTGCCCGAGACC 101
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                                                                                                             TCTCTGTCAATCCCTACCGAGACCTACAGATCTACAGCCGGCAGCATATGGAACGCTACC
                                                                                                                                                                                      AGAACCTCCGGCGGTTCCGGGAGAACCTCATTTATACCTACATCGGTCCTGTCCTAG
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ISGESGAGGTEATRIRLLOFY ABTOP APERGGAVED FLAGEN FLYEVAGUATURAVA
SRECKYNDYGEDEKGAPYGGHILSYLLEKSRVVHONHGERNEHVEYGLLEGGEETLR
RLGLERNEOSYLYLKGOCAKVSS INDKSDWKVKRKALSYIDFTEDEVEDELLSTVASV
ILLEQARTRODALKAVYSRTETYBLYRK ILLEKSRVTHONHGERNEHVEYGLLEGGEETLR
LHLGANIHERAADEDSNAOYTTEROLKYLTERLGYBESTTLREALTHIRK I IAKGEELLSPL
FOHNSFEOFCINYCNEKLOOLFIELTLKSDEDEKTARSTAREDYVGYENKKI I ODLYEE
KFKGI ISTLDEECLRPGEATDLTFLEKLEDTVK RHPHFLTHKLADOKTRKSLDRGEER
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LLHYAGEVTYSVTGFLDKNNDLLFRNLKETMCSSMNPIMAQCFDKSTRKSLDRGEER
LAGASKELLQLUELIRKSEPAYIRCIK PNDAKOPERDEVALUVEHLGVKYREBEYKMGRTKK I FI
RAFNKTLFATEDSLEVEROSLATKI QAAMRGFHBROKFLRVKRSAI CIOSWRGGTLGR
REPKTLFATEDSLEVEROSLATKI QAAMRGFHBROKFLRVKRSAI CIOSWRGGTLGR
PTPPPALREASELLRELGFILRHSPRCPENAFT LDHVARSFLLNLRGCLPRNVLDTSW
VERLF ISTRLIFGET LRHSPRCPENAFT LDHVARSFLINLRROLPRNVLDTSW
VERLF STRLGTEELSBRVLOSLGSBETOYANPVKYDRKGYKPRPROLLLTPSAVVI
LSADRVNNINININGSTTPAAGGRERDGIT TOFTGCTET I THK RWGGTT ANNA DEN NEDE
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	325	GTGGTGTCAGTTTCTATGAAGTACCACCTCATTTGTTTGCAGTGGCTGACACTGTATACC 3	84
	342 385	GGGCACTTCGTACTGAGCGTCGGGACCAGGCAGTGATGATTTCTGGAGAGAGTGGGGCAG 4	01 44
	402 445	GCAAGACAGAGGCCACCAAGAGAGACTGCTCCAGTTCTATGCAGAGAGACCTGCCCAGCCCCTG 4	61 04
	462 505	AACGGGGTGGCGAGTGCGAGACCGCCTGTTGCAGAGCAACCCCGTGTTAGAGGCCCTTTG 5	21
	522 565	GGAATGCCAAGACTCTCCGCAACGATAACTCCAGCCGGTTTGGAAAGTACATGGATGTGC 5	81 · · · · · · · · · · · · · · · · · · ·
	582 625	AGTTTGACTTCAAGGGTGCCCCCGTGGGAGGCCACATTCTCAGTTACCTCCTGGAAAAGT 6	41 84
	642 685	CCCGGGTGGTGCACCAAAATCACGGAGAGCGGAACTTCCACGTCTTTTACCAGCTACTGG 7	01
	702 745	AGGGGGGCGAGGAGACTCTCCGTCGGCTGGGCTTGGAACGGAACCCCCAGAGCTACT 7	61 04
	762 805	TGTACCTGGTGAAGGGCCAGTGTGCCAAGGTCTCCTCCATCAACGACAAGAGTGACTGGA 8	21 64
	822 865	AGGTTATGAGGAAGGCGCTGTCCGTCATTGACTTCACTGAGGATGAAGTGGAGGACTTGC 8   1111111111111111111111111111111111	81 24
	882 925	TCAGCATCGTGGCCAGCGTCCTACATCTGGGCAACATCCACTTTGCTGCTGACGAGGACA 9	41 84
	942 985	GCAATGCCCAGGTTACTACTGAGAACCAGCTCAAATATCTGAGCAGGCTCCTTGGTGTGG 1	001
	1002 1045	AAGGTACAACACTTAGGGAAGCCCTGACCCACAGGAAGATCATCGCCCAAGGGGGAAGAGC 1	061 104
	1062 1105	TCCTGAGCCCACTGAACCTTGAACAGGCGGCATATGCAAGGGATGCGCTTGCCAAGGCTG	121
	1122 1165	TGTACAGCCGGACATTCACCTGGCTGGTCAGAAAGATCAATAGGTCACTGGCCTCTAAGG 1	181 224
	1182 1225	ACGCTGAGAGCCCCAGCTGGCGAAGCACCACGGTTCTTGGGCTCCTGGACATTTACGGCT 1	241 284
	1242 1285	TTGAAGTGTTTCAGCATAACAGCTTCGAGCAGTTCTGCATCAACTACTGCAATGAGAAGC 1	301
	1302 1345	TGCAGCAGCTCTTCATCGAGCTGACTCTCAAGTCGGAGCAGGAGGAAGAATACGAGGCTGAGG 1	361
-	1362 1405	GCATCGCGTGGGAACCTGTCCAGTACTTCAACAACAACATCTCTGTGACCTGGTAGAGG 1	421

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2500 2544	41 CCCGGAATGTTCTGGACACCTCCTGGCCCACACCCCCACCTGCCCTGAGAGAGGCCTCAG	Qy 24. Db 24	
2484	- ATSCETTETTETTSACCAGETGEGGCETCATTTTTGETTACCTGAGCGGCAACTGC	. A. ∪	
42	5 AGACCATCCGTCGACTCATCCGGGCTTCATTTTGCGCCATTCACCCCGGTGCCCTGAGA	2 2	
2380	AGACCATCCGTCGACCCATCCGTGGCTTCATTTTGCGCCATTCACCCCGGTGCCCTGAGA	Оу 23	
2364	5 AGTCATGGTGGCGTGGCACACTGGGCCGGAGGAGGCAGCCAAGAGGAAGTGGGCAGCCC	23	
2320	AGTCATTGGTGGCGTGGCACACTGGGCCGGAGGAAGGAGGCCAAGAAGAGGAAGTGGGCAGCCC	22	
2304	5 GGAGGGCTTTCATTGGCGACAGAAATTTCTCCGGGTGAAGCGATCAGCCATCTGTATCC	22	
2	GGAGGGCTTTCATTGGCGACAGAAATTTCTCCGGGTGAAGCGATCAGCCATCTGTATCC	22	
2244	S CCACAGAGGACTCCCTGGAAGTCCGGCGGCAGCAGCTCTAGCCCACCAAGATCCAGGCGGCCT	$\vdash$	
	CCACAGAGGACTCCCTGGAAGTCCGGCGGCAGAGTCTAGCCACCAAGATCCAGGCGGCCT	21	
2184	CAGAAGAGTACAAAATGGGCAGGACTAAGATCTTCATCCGATTTCCCAAGACCTTGTTTG	21	
2140	1 CAGAAGAGTACAAAATGGGCAGGACTAAGATCTTCATCCGATTCCCCCAAGACCTTATTTTG	20	
2124	TGTGGGCAGGACGGCCCCAGGATGGTGGGCCGTGTTGGTCAGACACCTCGGCTACAAGC		
	1 TGTGGGCAGGACGCCCCAGGATGGTGGTGGCCGTGTTGGTTCAGACACCTCGGCTACAAGC		
2064	5 GTCGCAAATA	20	
2020	1 GTCGCAAATATGAGGCTTTCCTGCAGAGGTACAAGTCACTGTGCCCCAGAGACATGGCCCA	19	
2004	5 AGGTGAAGTACCTGGGACTGATGGAGAATCTGCGCGTGCGCAGAGCTGGCTTTGCCTATC	19	
1960	1 AGGTGAAGTACCTGGGACTGATGGAGAGATCTGCGCGCTGCGCAGAGCTGGCTTTGCCTATC	19	
1944	5 GCATCAAGCCAAACG	18	
1900	1 GCATCAAGCCAAACGACGCCAAGCCGGGTCGCTTTGATGAGGTGCTCATCCGACATC		
1884	25 AGATGAGCCTCCTGCAGCTCGTGGAGATCCTGAGGTCTAAGGAGCCTGCCT		
1840	1 AGATGAGCCTCCTGCAGCTCGTGGAGATCCTGAGGTCTAAGGAGCCTGCCT		
1824	5 GCTTTGACAAGAGTGAGCTCAGTGACAAGAAGCG		
1780	2 GCTTTGACAAGAGTGAGCTCAGTGACAAGAAGCGGCCAG-GACGGTGGCCACCCAGTTC		
1764	D5 TCCTCTTCCGGAACCTGAAGGAGACCATGTGCAGCTCAATGAACCCCATCATGGCCCAGT	Db 170	
1721	2 TCCTCTTCCGGAACCTGAAGGAGACCATGTGCAGCTCAATGAACCCCCATCATGGCCCAGT		
1704	15 TGCATTATGCTGGAGAGGTGACCTACAGTGTGACTGGGTTTCTGGATAAAAACAATGACC	Db 164	
1661	2 TGCATTATGCTGGAGAGGTGACCTACAGTGTGACTGGGTTTCTGGATAAAAACAATGAC	ý 1	
1644	5 CGCACAAGCTCGCTGACCAGAAAGACCAGGAAATCTCTAGACCGAGGGGAGTTCCGCCTTC	Ġ	
1601	2 CGCACAAGCTCGCTGACCAGAAGACCAGGAAATCCCTAGACCGAGGGGAGTTCCGCCTTC	15	
1584		Db 152	
	2 CGGACCTGACCTTTCTGGAGAAGTTGGAGGACACTGTCAAGCCCCACCCTCACTTCCTG	14	
1524	5 AGAAGTTCAAGGGCATCATCTCCATCTTGGATGAAGAGTGCCTGCGTCCTGGGGAGGCCA	14	
	2 AGAAGTTCAAGGGCATCATCTCCCATCTTGGATGAAGAGTGCCTGCGTCCTTGGGGAGGCCA	4	

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                            GAAGGCTTCAGTGGACCCCTCCTGACTCCTGATGCTTCGCTTAGTCCCCTCCCCTCC
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TCCGCCTTCTGCATTATGCTGGAGAGGTGACCTACAGTGTGACTGGGTTTCTGGATAAAA
                                          ACTTCCTGACGCACAAGCTCGCTGACCAGAAGACCAGGAAATCTCTAGACCGAGGGGAGT
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Clone distribution: NCI-CAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11296 row: n column: 11
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BI410257
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Tissue Procurement: Gilbert Smith,
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Contact: Robert St
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National Institutes of Health, Mammalian
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602966247F1 NCI_CGAP_Lu33
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Location/Qualifiers
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 907)
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                                                                                                                                                         Conservative
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                                     NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Ma
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
          Ph.D.
                             Email:
Tissue
                                                                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 858)
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Library Preparation:
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High quality sequence stop: 775.
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Clone distribution: MGC clone distribution information
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/clone_lib="NCI_CGAP_Mam4"
/tissue_type="tumor, gross t
/dev_stage="5 months"
/lab_host="DH10B"
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/strain="NMRI"
/db_xref="taxon:10090"
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BP 191 91006 EVRY cedex - France
Email: segrefégenoscope.cns.fr, Web : www.
Location/Qualifiers
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Full-Length cDNA libraries and normalization
Contact: Genoscope
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                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="B cells from Burkitt lymphoma"
/note="Vector: pcMvSPORT 6; Site_1: NotI; 1st strand cDNA
/note="Vector: pcMvSPORT 6; Site_1: NotI; 1st strand cDNA
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco Rv sites of the pcMvSPORT 6
Life Technologies. Contact: Feng Liang Life Technologies, Contact: Feng Liang Life Technologies,
Rockville, Maryland 20550, USA Fax: (1) 301 610 8371

http://e.iiiang@lifetech.com URL | Contact |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="cs0bL009YJ18"
/clone_lib="LTI_NFL010_BC2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="male"
                                                                                                                                                                                                                                                                                                      20.18;
                                                                                                                                                                                                                                                                 Score 737.6; DB 9;
Pred. No. 3.7e-178;
1; Mismatches 110;
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sapiens cDNA clone CS0DL009YJ18 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web : www.genoscope.cns.
                                                                                                                                                                                                                                                                                                                                                                         2 others
                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                           Length 939;
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REFERENCE
AUTHORS
TITLE
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SOURCE
                                                                                                                                                                               RESULT 5
BQ956845
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2351 TITTGGGCCATTCACCCCGGGTGCCCTGAGAATGCCTTCTTCTTGGACCACGTGCGCGCCT 2410
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                  house mouse.

M Mus musculus
Eukaryota; Metazoa; Chordata; Crar
Mammalla; Eutheria; Rodentia; Sciu
1 (bases 1 to 932)
NIH-MGC http://mgc.ncl.nih.gov/.
National Institutes of Health, Mar
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             539 TCCTGCGCCACGCCCCCCCGCCCGAGAACGCCTTCTTCCTGGACCATGTGCGCACCT 598
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                                                                                                                                                                                                                                 GCTCTGAACCCATCCAGTATGCCGTGCCCGTGGTAAAA 2748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121
Contact: Robert Strausberg, Ph. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                   CCGTGGCTAGTGAGATCTTCAAGGGCAAGAAGGATAATTACCCTCAGAGTGTACCCAGGC 838
                                                                                                                            BQ956845
BQ956845.1
                                                                                                                                                                                                                                                                                                                                              TGGTGTGGAAATACTGCCGGAGTATCAGCCCTGAGTGGAAGCAGCAGCTGCAGCAGCAGAAGG
                                                                                                                                                                                                                                                                                                                                                            TGGTGTGGAAGTACTGCCGGAGCATCAGCCCTGAGTGGAAGCAGCAGCAGCTGCAGCAAAAGG
                                                                                                                                                                                                                                                                                                                                                                                       CGCCCCCCTCCCTCCCTCAGGCCTTCAGAGCTTCTGCGGGAGTTGTGCATAAAGAACA 718
                                                                                                                                         B0956845

AGENCOURT 8800261 NCI_CGAP_CO24

IMAGE: 6399165 5', mRNA sequence.
                                                                                                                    EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGAAGGCAGCAAGAGGAAGTGGGCAGCCCAGACCATCCGTCGACTCATCCGTGGCTTCA 2350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGAGTCTAGCCACCAAGATCCAGGCGGCCTGGAGGGGCTTTCATTGGCGACAGAATTTC 2230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCGTGTTGGTCAGACACCTCGGCTACAAGCCAGAAGAGTACAAAATGGGCAGGACTAAGA 2110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCTTCATCCGCTTCCCCAAGACCCTGTTTGCCACAGAGGATGCCCTGGAGGTCCGGCGGC 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACAAGTCACTGTGCCCAGAGACGTGGCCCACGTGGGCAGGACGGCCGCA-GATGGGGTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACAAGTCACTGTGCCCAGAGACATGGCCCATGTGGGCAGGACGGCCCCAGGATGGTGTGG
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                                                                                                                         GI:22372323
                                                    Chordata; Craniata; Vertebrata; Euteleostomi;
Rođentia; Sciurognathi; Muridae; Murinae; Mus
                           Mammalian
                                                                                                                                    Mus musculus cDNA clone
                                                                                                                                                                 mRNA
                        Gene Collection
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42 CGGCCCTGGGCAGTGACCGGGGTTCGAGTGACCATGGAGAGCGCCCTTGACTGCCCGAGACC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCCGGGTGGTGCACCAAAATCACGGAGAGCGGAACTTCCACGTCTTTTACCAGCTACTGG
                                                                                                                                                                                                                                                                                                                                GCAAGACAGAGGCCACCAAGAGACTGCTCCAGTTCTATGCAGAGACCTGCCCAGCCCCTG
                                                                                                                                                                                                                                                                                                                                                                                                            GGGCACTTCGTACTGAGCGTCGGGACCAGGCAGTGATGATTTCTGGAGAGAGTGGGGCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCTCTGTCAATCCCTACCGAGACCTACAGATCTACAGCCGGCAGCATATGGAACGCTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGTAGGGGTGCAGGACTTTGTCCTGGAGAATTTCACCAGTGAGGCTGCCTTCATTG 161
                                                                     GGAATGCCAAGACTCTCCGCAACGATAACTCCAGCCGGTTTGGAAAGTACATGGATGTGC
                                                                                                                                                                                                                                                  AACGGGGTGGCGAGACCGCCTGTTGCAGAGCAACCCCGTGTTAGAGGCCTTTG
                                                                                                                                                                                                                                                                                                            GCAAGACAGAGGCCACCAAGAGACTGCTCCAGTTCTATGCAGAGACCTGCCCAGCCCCTG
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                                                                                                              AGTTTGACTTCAAGGGTGCCCCCGTGGGAGGCCACATTCTCAGTTACCTCCTGGAAAAGT 641
                                                                                                                                                  GGAATGCCAAGACTCTCCGCAACGATAACTCCAGCCGGTTTGGAAAGTACATGGATGTGC
                                                                                                                                                                                                                                AACGGGGTGGCGAGTGCGAGACCGCCTGTTGCAGAGCAACCCCGTGTTAGAGGCCTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGAACCTCCGGCGGCGGTTCCGGGAGAACCTCATTTATACCTACATCGGTCCTGTCCTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tissue Procurement: The Cepko Laboratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
LNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         quality sequence stop:
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cclone="IMAGE:6399165"
/clone_lib="NCI_CCAP_CC24"
/clone_lib="NCI_CCAP_CC24"
/lab_host="PH10B (T1 phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo d'
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 263 c 276 g 188 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /strain="FVB/N"
/db_xref="taxon:10090"
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Pred. No. 1.6e-174;
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AGGGGGGGGAGGAGGACTCTCCGTCGGCTGGGCTTGGAACGGAACCCCCAGAGCTACT 761

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ORGANISM
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                                                                                                                        Query Match
Best Local Similarity
                                                                                                Matches 744;
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                          1268 GAGCAGTTCTGCATCAACTACTGCAATGA-GAAGCTGCAGCAGCTGCTTCATCGAGCTGAC 1326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: Dr. James Lin, Univeristy of Iowa
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
cDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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UI-M-FCO-byb-f-07-0-UI.rl NIH_BMAP_FCO
IMAGE:5715846 5', mRNA sequence.
BO571422
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
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                                                                                                                                                                                                                 //lab.host="DHIOB (TI phage resistant)"
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//lab.host="Driver provided according to state..."
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//lab.host strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction.
//ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail
//ligated with coated between the Not I site and the polyA tail
//ligated provided by Notional Molecular Anatomy Project (BNAP): "Gene Discovery in the Developing Mouse Nervous System", supported by National Instututes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."
//lab.host="Propression of the polyA tail to there"
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/tissue_type="whole brain"
/dev_stage="embryo_12.5 dpc"
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Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTTCAACAACAAGATCATCTGTGACCTGGTAGAGGAGAAGTTCAAGGGCATCATCTCCAT
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Mammalla: Eutheria; Rodentia; Sciurognath
1 (bases 1 to 760)
NIH-MGC http://mgc.nci.nih.gov/.
Mational Institutes of Health, Mammalian
                                                                                                                                                                                        mRNA sequence.
B1665846
nttp://image.llnl.gov
                                                                                          Unpublished (1999)
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                     CCCTGAGAATGCCTTCTTGTTGGACCACGTGCGCGCCTCATTTTTGCTTAACCTGAGGCG
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/sex="female, virgin"
/tissue_type="infiltrating d
/dev_stage="5 months"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sai
Site_2: NotI; Cloned unidirectionally. Primer: Oligo of
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"
a 217 c 224 g 150 t
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/db_xref="taxon:10090"
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                                                                                        CATCATTGACTTCACATCGGGCTCAGAGCTTCTCATCACCAAGGCTAAGAATGGCCACCT 3125
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                GGCTGTGGTGGCCCCACGGCTGAATTCTCGGTGATGAAGGCTGCGGTGGACCGCTCCTGA 3185
GGCTGTGGTGGCCCCACGGCTGAATTCTCGGTGATGAAGGCTTCAGTGGACCCCCTCCTGA
                                                                     CATCATTGACTTCACATCGGGCTCAGAGCTTCTCATCACCAAGGCTAAGAATGGCCACCT
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13897 row: a column: 21
High quality sequence stop: 617.
Location/Qualifiers
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AGENCOURT_8815329 NCI_CGAP_Co24
IMAGE:6398108 5', mRNA sequence.
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Tissue Procurement: The Cepko Laboratory
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Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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BQ942930.1 GI:22358408
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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/clone="IMAGE:6398108"
/clone="ib="NCI_CGAP_CO24"
/clone=lib="NCI_CGAP_CO24"
/lab_host="DB10B (T1 phage-resistant)"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: SalI; Cloned unidirectionally. Primer: Oligo dn
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dn
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
a 271 c 245 g 197 t
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/strain="FVB/N"
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97.8%;
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                              http://image.llnl.gov
plate: LLAMI1744 row: d column:
                                                                                                                                                                                                                                                                                                                                                                                                                                   Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BI559061 817 bp mRNA linear EST 05-SEP-2001 603241534F1 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:5294168 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA Library Preparation: Life Technologies,
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall Site_2: NotI; Cloned unidirectionally. Primer: Oligo do Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Priscilla Furth, NIH Reference for transgenic model: Li et al., Cell Grow
                                                                                              /tissue_type="tumor, gross tissue"
/dev_stage="5 months"
/lab_host="DH10B"
                                                                                                                                                                                                           /organism="Mus musculus"
/strain="NMRI"
                                                                                                                                                                                                                                             1. .817
                                                                                                                                                    /clone_lib="NCI_CGAP_Mam4"
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/clone="IMAGE:5294168"
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                                   mRNA sequence.
B1653422
B1653422.1 GI:
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                                                 CCTGGTAGAGGAGAAGTTCAAGGGCATCATCTCCATCTTGGATGAAGAGTGCCTGCGTCC
                                                                                                                                                                                                        CATTTACGGCTTTGAAGTGTTTCAGCATAACAGCTTCGAGCAGTTCTGCATCAACTACTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs -r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
found through the I.M.A.G.E. Consortium or found through the I.M.A.G.E. Consortium (LLNL)
found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LLAM11867 row: d column: 17
                                                                                                                                                                                                                                                                                                             GGGGGAAGAGCTCCTGACCCCACTGAACCTTGAACAGGCGGCATATGCAAGGGATGCGCT
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Mammalia; Eutheria; Rodentia; Sc
1 (bases 1 to 763)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, M
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Mus musculus
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/tissue_type="tumor, gross tissue"
/dev_stage="10 months"
/lab_host="DH10B"
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/clone="IMAGE:5341408"
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98.3%;
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Sciurognathi; Muridae; Murinae; Mus
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                Query Match
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Matches 733;
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NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, i
                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-xia Dence CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
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BI156248
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602903422F1 NCI_CGAP_Mam3
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Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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Location/Qualifiers
                  Conservative
                                                                                                 /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies Investigators providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH Reference for transgenic model: Xu et al., Nature Genetics 22, 37-43 (1999)."
                                                                                                                                                                                                                                                  /strain="129,C57BL/6J,FVB/N"
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                                                                                                                                                                                          /tissue_type="tumor, gross tissue"
/dev_stage="10 months"
/lab_host="DH10B"
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                Score 709.8; DB 13
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                                                                                                                                                                                                                                                                                                                           AGCAGTTCTGCATCAAC
                                                                                                                                                                                         mRNA sequence.
BF538167
BF538167.1 GI
Contact: Robert Strausberg, Ph.D.
Email: cgapbs r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
cDNA Library Preparation: Life Technologies,
                                                                                                                                                                                                                                   BF538167
602053638F1 NCI_CGAP_SG2
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National Institutes of Health, Mammalian
                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                             Mus musculus
                                                           Unpublished (1999)
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               CAAGCAGAGAATTGATTATGCCAACCTAACCGGAATCTCTGTGAGTAGCCTGAGTGATAG
                                                                                                                             CTCTGAACCCATCCAGTATGCCGTGCCCGTGGTAAAATACGACCGTAAGGGTTACAAGCC
CAAGCAGAGAATTGATTATGCCAA-CTAACCGGAATCTCTGTCAGTAGCCTGAGTGATAG
                                                                               TCGCCCCGGCAGCTGCTGCTCACGCCCAGTGCTGTGGTGGTCATTGTGGAAGGATGCTAAAAGT
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DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://lmage.llnl.gov
plate: LLAM9524 row: k column: 09
H19h quality sequence stop: 748.
Location/Qualifiers
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/clone="NCI_CGAP_SG2"
/clone="NCI_CGAP_SG2"
/lab_host="OBIOB (TI phage-resistant)"
/note="Organ: sallvary gland; Vector: pCMV-SPORT6; Site_1: NOTI; Site_2: Sall; Cloned unidirectionally Primer: Oligo dT Average insert size 1.3 kb. Constructed by Life Technologies. Note: this is a NCI_CGAP Library."
a 242 c 242 g 177 t
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/strain="FVB/N"
/db_xref="taxon:10090"
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Pred. No. 7.9e-171;
0; Mismatches 30;
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TCTCTGTCAATCCCTACCGAGACCTACAGATCTACAGCCGGCAGCATATGGAACGCTACC
                                                                                                                                                GGGTAGGGGTGCAGGACTTTGTCCTGCTGGAGAATTTCACCAGTGAGGCTGCCTTCATTG
                                                               AGAACCTGCGGCGATTTCGGGAGAATCTCATCTACACCTACATTGGCCCCGTCCTGG
                                                                                AGAACCTCCGGCGGCGGTTCCCGGGAGAACCTCATTTATACCTACATCGGTCCTGTCCTAG
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BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Li,W.B., Gruber,C., Jessee,
Full-length cDNA libraries
Unpublished (2001)
Contact: Genoscope
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1 (bases 1 to 930)
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//Issue_type="placenta"
//Issue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com"
2088 g 167 t 2 others
                                                                                                                                                                                                                                                                Conservative
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/db_xref="taxon:9606"
/clone="CSODIO30YD16"
/clone_lib="LTI_NFL006_PL2"
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Pred. No. 1.3e-168;
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AGENCOURT_6393520 NIH_MGC_72 Homo
5', mRNA sequence.
BM450184
        Contact: Robert Strausberg, Ph.D.
Email: cgapbs r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
Clone distribution: MGC clone distribution information
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM12204 row: 1 column: 20
                                                                                                                         National Institutes of Health, Mammalian Unpublished (1999)
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                                                    CCCCAAGACCTTATTTGCCACAGAGGACTCCCTGGAAGTCCGGCGGCAGAGTCTAGCCAC
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                                        TCCCAAGACCCTGTTTGCCACAGAGGATGCCCCTGGAGTCCCGGGGGAGAGCCTGGGCAC
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone_lib="NMAGE:5528227"
/clone_lib="NHI_MGC_72"
/tissue_type="melanotic melanoma"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: Not Site_2: Sall; Cloned unidirectionally. Primer: Olic Site_2: Sall; Cloned unidirectionally. Primer: Olic Average insert size 2 kb. Library constructed by 1 Technologies."
Technologies."
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Pred. No. 2.7e-163;
0; Mismatches 127;
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TCCTCCGGGTGAAGAGATCAGCCATCTGCATCCAGTCGTGGTGGCGTGGAACACTGGGCC
                     TTCTCCGGGTGAAGCGATCAGCCATCTGTATCCAGTCATGGTGGCGTGGCACACTGGGCC
                                                                                                                                        AGATCTTCATCCGATTCCCCAAGACCTTATTTGCCACAGAGGACTCCCTGGAAGTCCGGC
                                                                     GCCAGAGCCTGGCCACAAAGATCCAAGCTGCCTGGAGGGGCCTTTCACTGGCGGCAGAAT
                                                                                          GGCAGAGTCTAGCCAACCAAGATCCAGGCGGCCTGGAGGGGGCTTTCATTGGCGACAGAAAT
                                                                                                                                                                                                                      806;
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BQ958694.1
EST.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bloscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM258 row: m column: 06
High quality sequence stop: 635.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; 1 (Dases 1 to 1068)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
Contact: Robert Strausberg,
                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                          /tissue_type="carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: prostate; Vector: pOTB7; Site_1: XhoI;
/site_2: EcoRI, cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Supersoript II RT (Life Technologies).

Note: this is a NIH_MGC Library."
1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6479885"
/clone_lib="NIH_MCC_40"
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85.0%;
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                                                                                                                                                                                                             Score 679.4; DB 14; pred. No. 3.5e-163; 0; Mismatches 137;
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CGGTGAAAGCATCACCATCAGCAGGGGCAGCATCACCGTTTGCAGGGG
                                                                 TGCTGCAGAGTGATCA-TGTGATCGAGACACTAACCAAGACGGCCCTCAGTGCTGACC-G
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                                                   TGCTGCAAAGTGACCACCGTGATGGAGACGCTGACCAAGACAGCCCTCAATGGCAACCGG
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Search completed: December 9, 2002, 15:10:49 Job time: 3255 secs

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Tue Dec 10 09:26:42 2002
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                                                        December
                                                                                                                                                                          GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd
9, 2002, 15:10:56; search time 67 seconds (without alignments) 2076.323 Million cell updates/sec
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Title: Perfect score: US-09-893-371-1 5398 1 MRV"

Sequence: MRYRASALGSDGVRVTMESA.....LITKAKNGHLAVVAPRLNSR 1044

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Maximum Minimum DB seq length: 0
DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database A\_Geneseq\_101002:\*

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Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being part and is derived by analysis of the total score distribution. printed ۵

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1685	14.5	38.5	70.5	1782	00.5	2378	3369	65.5	5216	Score
31.2	31.8	32.2	32.8	33.0	33.4	44.1	62.4	95.7	96.6	Query Match L
909	1098	1026	697	700	1011	537	935	1050	1063	Length DB
22	23	22	22	22	22	22	22	22	22	:
AAU23128	AAU97544	AAU23125	AAB64616	AAB64615	ABB71113	AAM4 1777	ABG10172	ABG10171	ААМ39991	ID
Novel human enzyn	Human Myosin-1F	Novel human enzy	Human secreted p	Human secreted pro	Drosophila melan	Human polypeptid	Novel human diag	Novel human diag	Human polypeptid	Description

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	31	30													17	16	15	14	13	12	11
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1972	1988	1988	2056	1963	1960	1879	631	1120	1469	569	1453	1939	753	697	764	1839	1804	1769	1754	2057	2048	1495	1556	1505	2424	2058	1483	1544	1493	2129	512	2167	759	1089
17	22	22	22	22	22	22	17	21	22	21	22	23	22	17	22	21	21	21	21	22	22	21	21	21	22	23	21	21	21	22	21	22	22	23
AAW00024	AAM41000	ААМ4 0999	ABB59344	ААМ79838	AAM78854	AAM25750	AAW00604	AAY94292	.AAM39214	AAB57005	ААМ39213	ABB77096	AAM79139	AAW00603	AAM80123	AAY94291	AAG52408	AAG52409	AAG52410	AAE11890	AAE11891	AAG30440	AAG30438	AAG30439	ABB58924	ABB97219	AAG48640	AAG48638	AAG48639	ABB62828	AAB42651	ABB60369	61	ABB97258
Smooth muscle myos		Human polypeptide	phila mel	protein	Human protein SEQ	Human protein sequ	Murine myosin VII	Helianthus annuus							Human protein SEQ	rt			ᡤ		ຜ	Arabidopsis thalia	Arabidopsis thalia	Arabidopsis thalia	Drosophila melanog	Novel human protei	Arabidopsis thalia		CO.	Drosophila melanog		Drosophila melanog	human	Novel human protei

## ALIGNMENTS

AMIN 3 9 3 1 ;	22-OCT-2001 (first entry) .	Human polypeptide SEQ ID NO 3136.	; nootropic; immunosuppressant; cytostatic; gene	mokinetic; thrombolytic; drug screening; arthritis	chemokinetic; thrombolytic; drug screening; arthritis leukaemia.	nokinetic; thrombolytic; drug screening; arthritis caemia. ) saplens.	mokinetic; thrombolytic; drug screening; arthritis seemia. Saplens.	mokinetic; thrombolytic; drug screening; arthritis semia. saplens.	mokinetic; thrombolytic; drug screening; arthritis kaemia.  S sapiens.  00153312-A1.  JUL-2001.	<pre>chemokinetic; thrombolytic; drug screening; arthritis leukaemia. Homo sapiens. WO200153312-A1. 26-JUL-2001. 26-JUL-2000; 2000WO-US34263.</pre>
		rst entry)	rsc entry) . He SEQ ID NO 3136.	le SEQ ID NO 3136.  le SEQ ID NO 3136.  immunosuppressant; cytostatic; gene thous system; neuropathy; central nervous sixinson's disease; Huntington's disease; sral sclerosis; Shy-Drager Syndrome; chem prombolytic; drug screening; arthritis; i	le SEQ ID NO 3136.  le SEQ ID NO 3136.  immunosuppressant; cytostatic; gene therapy;  us system; neuropathy; central nervous system;  kinson's disease; Huntington's disease; haemos  gral sclerosis; Shy-Drager Syndrome; chemotacti  prombolytic; drug screening; arthritis; inflamm	le SEQ ID NO 3136. le SEQ ID NO 3136. ; immunosuppressant; cytostatic; gene thous system; neuropathy; central nervous skinson's disease; Huntington's disease; ral scherosis; Shy-Drager Syndrome; chen urombolytic; drug screening; arthritis; i	le SEQ ID NO 3136.  le SEQ ID NO 3136.  immunosuppressant; cytostatic; gene tlus system; neuropathy; central nervous; kinson's disease; Huntington's disease; ral sclerosis; Shy-Drager Syndrome; cheurombolytic; drug screening; arthritis;	le SEQ ID NO 3136.    immunosuppressant; cytostatic; gene thus system; neuropathy; central nervous; kinson's disease; Huntington's disease; ral sclerosis; Shy-Drager Syndrome; chemicombolytic; drug screening; arthritis;	le SEQ ID NO 3136.  ; immunosuppressant; cytostatic; gene tius system; neuropathy; central nervous; kinson's disease; Huntington's disease; ral sclerosis; Shy-Drager Syndrome; cheurombolytic; drug screening; arthritis;	le SEQ ID NO 3136.  le SEQ ID NO 3136.  ; immunosuppressant; cytostatic; gene tius system; neuropathy; central nervous; kinson's disease; Huntington's disease; kinson's disease; system sclerosis; Shy-Drager Syndrome; cheurombolytic; drug screening; arthritis; 10000-US34263.
001 (first entry) lypeptide SEQ ID NO 3136. sotropic; immunosuppressant; cytostatic; gene th	<pre>polypeptide SEQ ID NO 3136. nootropic; immunosuppressant; cytostatic; gene th</pre>	nootropic; immunosuppressant; cytostatic; gene th		Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; lankacmia	imer's; Parkinson's disease; Huntington's disease; rophic lateral sclerosis; Shy-Drager Syndrome; chenkinetic; thrombolytic; drug screening; arthritis; jemia.	imer's; Parkinson's disease; Huntington's disease; rophic lateral sclerosis; Shy-Drager Syndrome; chenkinetic; thrombolytic; drug screening; arthritis; jemia.	imer's; Parkinson's disease; Huntington's disease; rophic lateral sclerosis; Shy-Drager Syndrome; cherkinetic; thrombolytic; drug screening; arthritis; emia.  saplens.  153312-A1.	<pre>imer's; Parkinson's disease; Huntington's disease; rophic lateral sclerosis; Shy-Drager Syndrome; cher kinetic; thrombolytic; drug screening; arthritis; emia. saplens.</pre>	<pre>inder's; Parkinson's disease; Huntington's disease; irophic lateral sclerosis; Shy-Drager Syndrome; cheikinetic; thrombolytic; drug screening; arthritis; emia. saplens. 153312-A1.</pre>	<pre>imer's; Parkinson's disease; Huntington's disease; rophic lateral sclerosis; Shy-Drager Syndrome; cher kinetic; thrombolytic; drug screening; arthritis; emia. saplens. saplens. fl-2001. fl-2000; 2000WO-US34263.</pre>
001 (first entry)  lypeptide SEQ ID NO 3136.  ootropic; immunosuppressant; cytostatic; gene that nervous system; neuropathy; central nervous s	<pre>polypeptide SEQ ID NO 3136. nootropic; immunosuppressant; cytostatic; gene theral nervous system; neuropathy; central nervous system;</pre>	<pre>nootropic; immunosuppressant; cytostatic; gene theral nervous system; neuropathy; central nervous s</pre>	heral nervous system; neuropathy; central nervous s	amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic chemokinetic; thrombolytic; drug screening; arthritis; inflamma	<pre>trophic lateral sclerosis; Shy-Drager Syndrome; chen okinetic; thrombolytic; drug screening; arthritis; i aemia.</pre>	trophic lateral sclerosis; Shy-Drager Syndrome; chemokinetic; thrombolytic; drug screening; arthritis; jaemia.	trophic lateral sclerosis; Shy-Drager Syndrome; cherokinetic; thrombolytic; drug screening; arthritis; aemia. sapiens. 0153312-A1.	trophic lateral sclerosis; Shy-Drager Syndrome; cherokinetic; thrombolytic; drug screening; arthritis; aemia. sapiens.	trophic lateral sclerosis; Shy-Drager Syndrome; chenokinetic; thrombolytic; drug screening; arthritis; aemia. sapiens. 0153312-A1.	trophic lateral sclerosis; Shy-Drager Syndrome; chemokinetic; thrombolytic; drug screening; arthritis; aemia. sapiens. 0153312-A1. UL-2001. EC-2000; 2000WO-US34263.
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OOl (first entry)  lypeptide SEQ ID NO 3136.  cotropic; immunosuppressant; cytostatic; gene the land nervous system; neuropathy; central nervous: r's; Parkinson's disease; Huntington's disease; hic lateral sclerosis; Shy-Drager Syndrome; cheuetic; thrombolytic; drug screening; arthritis; a.  iens.  312-A1.  0001.	polypeptide SEQ ID NO 3136.  nootropic; immunosuppressant; cytostatic; gene theral nervous system; neuropathy; central nervous system; neuropathy; central nervous system; neuropathy; central nervous; disease; Huntington's disease; ophic lateral sclerosis; Shy-Drager Syndrome; cheinetic; thrombolytic; drug screening; arthritis; mia.  53312-A1.  53312-A1.	nootropic; immunosuppressant; cytostatic; gene theral nervous system; neuropathy; central nervous; mer's; Parkinson's disease; sophic lateral sclerosis; Shy-Drager Syndrome; chemia.  thrombolytic; drug screening; arthritis; appiens.  53312-A1.  -2000; 2000WO-US34263.	heral nervous system; neuropathy; central nervous : hmer's; Parkinson's disease; Huntington's disease; cophic lateral sclerosis; Shy-Drager Syndrome; chekinetic; thrombolytic; drug screening; arthritis; appiens.  153312-A1.  1-2001.	o sapiens. 00153312-A1. JUL-2001. DEC-2000; 2000WO-US34263.	WO200153312-A1. 26-JUL-2001. 26-DEC-2000; 2000WO-US34263.	лиг-2001. DEC-2000; 2000WO-US34263.	TUL-2001. DEC-2000; 2000WO-US34263.	DEC-2000; 2000WO-US34263.	CEC BOOK CONTROL	
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OOl (first entry)  lypeptide SEQ ID NO 3136.  lypeptide SEQ ID NO 3136.  cotropic; immunosuppressant; cytostatic; gene tal nervous system; neuropathy; central nervous r's; Parkinson's disease; Huntington's disease; hic lateral sclerosis; Shy-Drager Syndrome; cheetic; thrombolytic; drug screening; arthritis; en.  lens.  312-A1.  000. 2000WO-US34263.  000; 2000WS-058042.  000; 2000US-058042.	polypeptide SEQ ID NO 3136.  nootropic; immunosuppressant; cytostatic; gene teral nervous system; neuropathy; central nervous mer's; Parkinson's disease; Huntington's disease; ophic lateral sclerosis; Shy-Drager Syndrome; cheinetic; thrombolytic; drug screening; arthritis; apiens.  2001.  2000; 2000WO-US34263.  2000; 2000WS-0488725.  2000; 2000WS-0488725.  2000; 2000WS-0598042.	nootropic; immunosuppressant; cytostatic; gene teral nervous system; neuropathy; central nervous mer's; Parkinson's disease; Huntington's disease; cophic lateral sclerosis; shy-Drager Syndrome; cheinetic; thrombolytic; drug screening; arthritis; maplens.  13312-A1.  1-2000; 2000WO-US34263.  1-2000; 2000WS-0488725.  1-2000; 2000WS-0552317.  1-2000; 2000US-0598042.  1-2000; 2000US-0520312.	neral nervous system; neuropathy; central nervous iner's; Parkinson's disease; Huntington's disease; cophic lateral sclerosis; Shy-Drager Syndrome; che kinetic; thrombolytic; drug screening; arthritis; maia.  saplens.  153312-A1.  1-2001.  2-2000; 2000WO-US34263.  N-2000; 2000WS-0488725.  N-2000; 2000US-058317.  1-2000; 2000US-0553317.  1-2000; 2000US-05398042.  1-2000; 2000US-05398042.  1-2000; 2000US-0530312.	> ⋅	>					
OOl (first entry)  lypeptide SEQ ID NO 3136.  lypeptide SEQ ID NO 3136.  cotropic; immunosuppressant; cytostatic; gene to cotropic; immunosuppressant; cytostatic; gene to cotropic; immunosuppressant; cytostatic; gene to cotropic immunosuppressant; central nervous r's; Parkinson's disease; Huntington's disease; hic lateral sclerosis; Shy-Drager Syndrome; che etic; thrombolytic; drug screening; arthritis; e.  lens.  iens.  312-A1.  000; 2000WO-US34263.  000; 2000WS-0488725.  000; 2000WS-055317.  000; 2000WS-055317.  000; 2000WS-0553450.	polypeptide SEQ ID NO 3136.  nootropic; immunosuppressant; cytostatic; gene teral nervous system; neuropathy; central nervous mer's; Parkinson's disease; Huntington's disease; pophic lateral sclerosis; Shy-Drager Syndrome; cheinetic; thrombolytic; drug screening; arthritis; mia.  aplens.  53312-A1.  -2000; 2000WO-US34263.  -2000; 2000WS-0552317.  -2000; 2000US-0598042.  -2000; 2000US-0598043.	nootropic; immunosuppressant; cytostatic; gene teral nervous system; neuropathy; central nervous system; neuropathy; central nervous emer's; parkinson's disease; Huntington's disease; ophic lateral sclerosis; Shy-Drager Syndrome; cheinetic; thrombolytic; drug screening; arthritis; mapiens.  1.2001.  1.2001.  1.2000; 2000WO-US34263.  1.2000; 2000WS-0488725.  1.2000; 2000WS-0552317.  1.2000; 2000WS-0553450.	neral nervous system; neuropathy, central nervous liner's; Parkinson's disease; Huntington's disease; cophic lateral sclerosis; Shy-Drager Syndrome; che kinetic; thrombolytic; drug screening; arthritis; ania.  sapiens.  153312-A1.  L-2001.  2-2000; 2000WO-US34263.  R-2000; 2000US-0488725.  R-2000; 2000US-0553317.  L-2000; 2000US-05598042.  L-2000; 2000US-05598042.  L-2000; 2000US-05598042.  L-2000; 2000US-05598042.	> . ∵	>					
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OOl (first entry)  lypeptide SEQ ID NO 3136.  lypeptide SEQ ID NO 3136.  cotropic; immunosuppressant; cytostatic; gene tal nervous system; neuropathy; central nervous r's; Parkinson's disease; Huntington's disease; hic lateral sclerosis; Shy-Drager Syndrome; cheetic; thrombolytic; drug screening; arthritis; a.  iens.  312-A1.  0001.  0000; 2000WO-US34263.  0000; 2000WS-0488725. 0000; 2000WS-0582317. 0000; 2000WS-0582317. 0000; 2000WS-0598042. 0000; 2000WS-0598045. 0000; 2000WS-0593036.	polypeptide SEQ ID NO 3136.  nootropic; immunosuppressant; cytostatic; gene teral nervous system; neuropathy; central nervous mer's; Parkinson's disease; Huntington's disease; ophic lateral sclerosis; Shy-Drager Syndrome; che inetic; thrombolytic; drug screening; arthritis; apiens.  2001.  2000; 2000WO-US34263.  2000; 2000WS-0488725.  2000; 2000WS-0583436.  2000; 2000WS-0563456.  2000; 2000WS-0563456.  2000; 2000WS-0693036.	nootropic; immunosuppressant; cytostatic; gene teral nervous system; neuropathy; central nervous system; neuropathy; central nervous system; neuropathy; central nervous ophic lateral sclerosis; shy-Drager Syndrome; cheinetic; thrombolytic; drug screening; arthritis; aplens.  53312-A1.  53312-A1.  -2001, 2000W5-0488725.  -2000; 2000W5-058042.  -2000; 2000W5-052317.  -2000; 2000W5-052312.  -2000; 2000W5-052312.  -2000; 2000W5-052313.  -2000; 2000W5-052313.	neral nervous system; neuropathy; central nervous limer's; Parkinson's disease; Huntington's disease; rophic lateral sclerosis; Shy-Drager Syndrome; che kinetic; thrombolytic; drug screening; arthritis; maia.  sapiens.  153312-A1.  L-2001.  L-2000; 2000WO-US34263.  N-2000; 2000US-0488725.  R-2000; 2000US-0552317.  L-2000; 2000US-0552317.  L-2000; 2000US-0552317.  L-2000; 2000US-0552317.  L-2000; 2000US-053450.  P-2000; 2000US-0630312.  R-2000; 2000US-0630313.  R-2000; 2000US-0630313.  R-2000; 2000US-0630313.	> .	>					

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Best Local Sim
Matches 1003;
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            DLTFLEKLEDTVKPHPHFLTHKLADQKTRKSLDRGEFRLLHYAGEVTYSVTGFLDKNNDL
                                                                                                                                                                                  YLVKGQCAKVSSINDKSDWKVMRKALSVIDFTEDEVEDLLSIVASVLHLGNIHFAADEDS
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                                                         QQLFIELTLKSEQEEYEAEGIAWEPVQYFNNKIICDLVEEKFKGIISILDEECLRPGEAT
                                                                                         NAQVTTENQLKYLTRLLGVEGTTLREALTHRKIIAKGEELLSPLNLEQAAYARDALAKAV
                                                                                                                                                                                                                                             FDFKGAPVGGHILSYLLEKSRVVHQNHGERNFHVFYQLLEGGEEETLRRLGLERNPQSYL
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system injuries -
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New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess biodiversity.
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23-AUG-2000;
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2000US-0649167
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medical imaging; diagnostic; genetic disorder.
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mutations

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for identifying expressed genes. (I) is useful in gene therapy techniques (II) (II) (II) is useful for generating antibodies against it, detecting or cyanntitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC diagnostics, forensics, gene mapping, identification of mutations cresponsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences. ABG00010-ABG30377 represent novel human CC diagnostic amino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at fifth, wipo.int/pub/published_pct_sequences.
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                           IKPNDAKQPGREDEVLIRHQVKYLGLMENLRVRRAGEAYRRKYEAFLQRYKSLCPETWPM
                                                                                                LFRNLKETMCSSMNPIMAQCFDKSELSDKKRPETVATQFKMSLLQLVEILRSKEPAYIRC
                                                                                                                                                                     DLTFLEKLEDTVKHHPHFLTHKLADQRTRKSLGRGEFRLLHYAGEVTYSVTGFLDKNNDL
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation prolymerase chain reaction (PCR) primers, oligomers, and for and gene mapping, and in recombinant production of (II). The
                                                                                                                                                                                                                                                                                  New isolated polynucleotide and encoded polypeptides, useful diagnostics, forensics, gene mapping, identification of mutar responsible for genetic disorders or other traits and to assume the disorders of the contract of th
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CC diagnostic amino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at free with the printed control of the invention.
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Best Local :
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                                                                                        LLRELCIKNMVWKYCRSISPEWKQQLQQKAVASEIFKGKKDNYPQSVPRLFISTRLGTDE
                                              LLRELCMKNMVWKYCRSISPEWKQQLQQKAVASETFKGKKDNYPOSVPRLFISTRLGTEE
ISPRVLQSLGSEPIQYAVPVVKYDRKGYKPRPRQLLLTPSAVVIVEDAKV
                                                                                                                                                          TEDALEVRRQSL---
                                                                                                                                                                       TEDSLEVRROSLATKIQAAWRGFHWRQKFLRVKRSAICIQSWWRGTLGRRKAAKRKWAAQ
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62; Conservative
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Pred. No. 6.2e-278;
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Query Match Best Local Similarity

44.18; 96.78;

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2378; No. 9

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Length

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RESULT 4
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                                                  The invention relates to human nucleic acids (AA157798-AA161369) and the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: Immune system suppression, Activin/inhibin activity, chemotactic/chemokinctic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemias and
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25-APR-2000;
09-JUL-2000;
19-JUL-2000;
03-AUG-2000;
                       Note: The sequence specification.
 Sequence
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Zhao
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19-OCT-2000;
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Wang z
Zhou
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2000US-0552317.
2000US-05598042.
2000US-0620312.
2000US-06521450.
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2000US-0693036.
2000US-0727344.
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Wehrman T, X
Goodrich R,
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                                                                                                                                                                                                                                                                                                                 Drosophila; developmental biology; cell signalling; insecticide;
                      Disclosure; SEQ ID NO
                                                        New isolated nucleic acid
genes from Drosophila and
                                                                                                                             Venter JC,
                                                                                                                                                   (PEKE ) PE CORP NY
                                                                                                                                                                         23-MAR-2000;
11-JUL-2000;
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                                                                                                                                                                                                                                   27-SEP-2001.
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||:||||||| |||||||| 239
|KTDATKRLLQLYAETCPAPQRGGAVRDRLLQSNPVLEAFGNAKTLRNDNSSREGKYMDVQ 239
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)B; ABL15216.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                        GVAVLVRHLGYKPEEYKMGRTKIFIRFPKTLFATEDSLEVRRQSLATKIQAAWRGFHWRQ
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                                                                                                                                                                                                                                                                                                                                                                     HFLTHKLADQKTRKSL-DRGEFRLLHYAGEVTYSVTGFLDKNNDLLFR-----NLKET 554
                                                                                                                                                                                                                                                                                                                                                                                                                                          EAEGIAWEPVQYFNNKIICDLVEEKFKGIISILDEECLRPGEATDLTFLEKLEDTVKPHP 502
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                               RASFLLNLRRQL--PRNVLD----TSWPTPPPALREASELLR---ELCMKNMV-WKYCRS 843
                                                                                                  KFLRVKRSAICIOSWWRGTLGRRKAAKRKWAAQTIRRLIRGFILRHSPRCPENAFFLDHV 793
                                                                                                                                     GVRVLIEEKKF-AQDVKYGHTKIFIRSPRTLFALEHQRNEMIPHIVTLLQKRVRGWIVRR
                                                                                                                                                                                                         STVFDEERVEHQVRYLGLLENLRVRRAGFVHRQRYDKFLLRYKMISQYTWPNFRAGSDRD
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-SYVQELANRLRKAKQMRDYGKSIQWPQPPLAGRKVEAKLHRMFDFWRANMILHKYPRS
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CC The invention relates to the isolation of genes AAF32757-F32803 encoding CC the human secreted proteins AAB64549-B64594. The sequence is a search CC result from a BLASTX homology search. The genes and proteins are useful CC for preventing, ameliorating or treating medical conditions, e.g. by CC protein or gene therapy. The genes are isolated from a range of human CC antibodies and (antibogonists are useful in the diagnosis, treatment CC antibodies and (antibogonists are useful in the diagnosis, treatment CC other cancers of the adrenal gland, bone, bone marrow, breast, CC and prevention of: (a) cancer, e.g. breast and ovarian cancer, and CC gastrointestinal tract, liver, lung, or urogenital; (b) immune CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound CC and (f) infectious diseases such as viral, bacterial, fungal and
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                  healing; (e) neurocoand (f) infectious diseases
                                                                                                                                                                                                                                                                                                                            Disclosure; Page 516-518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disord neurological disease; infection; human; secreted protein.
                                                                                                                                                                                                                                                                                                                                                                           Isolated nucleic acid molecule
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                                                             RFDEVLIRHQVKYLGIMENLRVRRAGFAYRRKYEAFIQRYKSLCPETWPWWAGRPQDGVA
VLFNELEIPVEEHSFGRSKIFIRNPRTLFQLED
                      VLVRHLGYKPEEYKMGRTKIFIRFPKTLFATED
                                               IFNESIVCHQIRYLGILENVRVRRAGYAFRQAYEPCLERYKMLCKQTWPHWKGPARSGVE
                                                                                                  DHSLIKSLFPEGNPAKVNLKRPPTAGSQFKASVATLMRNLQTKNPNYIRCIKPNDKKAAH
                                                                                                                    MNPIMAQCEDKSELS--DKKRPETVATQFKMSLLQLVEILRSKEPAYIRCIKPNDAKQPG
                                                                                                                                                      HQHFESRMSKCSRFLNDTTLPHSCFRIQHYAGKVLYQVEGFVDKNNDLLYRDLSQAMWKA
                                                                                                                                                                                                                                                                                                                 RPASVK-VVLERAFSFRTVEAKREKVSTTLNVAQAYYARDALAKNLYSRLFSWLVNRINE
                                                                                                                                                                       HPHFLTH--KLADQKTRKSLDRGEFRLLHYAGEVTYSVTGFLDKNNDLLFRNLKETMCSS
                                                                                                                                                                                                          EYIREDIEWTHIDYFNNAIICDLIENNTNGILAMLDEECLRPGTVTDETFLEKLNQVCAT
                                                                                                                                                                                                                           EYEAEGIAWEPVQYFNNKIICDLVEEKFKGIISILDEECLRPGEATDLTFLEKLEDTVKP
                                                                                                                                                                                                                                                              SIKAQTKVRKK-----VMGVLDIYGFEIFEDNSFEQFIINYCNEKLQQIFIELTLKEEQE
                                                                                                                                                                                                                                                                              SLASKDAESPSWRSTTVLGLLDIYGFEVFQHNSFEQFCINYCNEKLQQLFIELTLKSEQE 440
                                                                                                                                                                                                                                                                                                                                          RLLGVEGTTLREALTHRKIIAKGEELLSPLNLEQAAYARDALAKAVYSRTFTWLVRKINR
                                                                                                                                                                                                                                                                                                                                                                     TVRNAMQIVGFLDHEAEAVLEVVAAVLKLGNIEFKPESRVNGLDESKIKDKIELNEKFAS
                                                                                                                                                                                                                                                                                                                                                                                      RVVHQNHGERNFHVFYQLLEGGEEETLRRLGLERNPQSYLYLVKGQCAKVSSINDKSDWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GVSFYEVPPHLFAVADTVYRALRTERRDQAVMISGESGAGKTEATKRLLQFYAETCPAPE 146
                                                                                                                                                                                                                                                                                                                                                                                                                         RVVKQPRGERNFHVFYQLLSGASEELLYKLKLERDFSRYNYL-SLDSAKVNGVDDAANFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EVNQVKEQLLQSNPVLEAFGNAKTVRNDNSSRFGKYMDIEFDFKGDPLGGVISNYLLEKS 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RGGAVRDRLLQSNPVLEAFGNAKTLRNDNSSRFGKYMDVQFDFKGAPVGGHILSYLLEKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IGVGDMVLLEPL-NEETFIDNLKKRFDHNEIYTYIGSVVISVNPYRSLPIYSPEKVEDYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NRNFYELSPHIFALSDEAYRSLRDQDKDQCILITGESGAGKTEASKLVMSYVAAVCGKGA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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51.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1782;
Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 22;
9.7e-143;
nes 203;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       700;
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AAB64616
ID AAB6
22-MAR-2001
                                                AAB64616 standard;
                                  (first entry)
                                               Protein;
                                                697
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secreted

protein

BLAST search protein SEQ ID

NO: 126,

Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disord neurological disease; infection; human; secreted

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The invention relates to the isolation of genes AAF32757-F32803 encoding C the human secreted proteins AAB64549-B64594. The sequence is used as a query sequence for doing BLASTX searches to identify homologous sequences. The genes and proteins are useful for preventing, cameliorating or treating medical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and can be specification. The nucleic acids, proteins, antibodies and can be specification. The nucleic acids, proteins, antibodies and can be specification. The nucleic acids, proteins, antibodies and can be specification. The nucleic acids, proteins, antibodies and can be specificated and ovarian cancer, and other cancers of the cancer, e.g. breast and ovarian cancer, and other cancers of the carenal gland, bone, bone marrow, breast, gastrointestinal cancers tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's cancers, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, crheumatoid arthritis and ulcerative colltis; (c) cardiovascular collisorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) collisorders and be such as wirely acceptant and proteins of the cancer and proteins diseases e.g. cerebral anoxia and epilepsy; and (f) collisorders and be such as wirely acceptant and proteins disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
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(ROSE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 519-521; 558pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-032312/04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2000; 2000WO-US14934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200077197-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated nucleic acid molecule encoding a human secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         infections
                                                                                                                                                                                                                                                                                                                                    134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nfectious diseases such as viral, bacterial, fungal and parasitic
                      357
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                                                                                                                                                                                                                                                                                                                                                                                                                                               GVSFYEVPPHLFAVADTVYRALRTERRDQAVMISGESGAGKTEATKRLLQFYAETCPAPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VGVQDFVLLENFTSEAAFIENLRRRFRENLIYTYIGPVLVSVNPYRDLQIYSRQHMERYR 86
                                                                                                                                                                                               Ħ
                                      RTFTWLVRKINRSLASKDAESPSWRSTTVLGLLDIYGFEVFQHNSFEQFCINYCNEKLQQ
                                                                                                                    GTTLREALTHRKI-------IAKGEELLSPLNLEQAAYARDALAKAVYS
                                                                                                                                                                             TVRNAMQIVGFMDHEAESVLAVVAAVLKLGNIEFKPE-----
                                                                                                                                                                                                                                                      RVVKQPRGERNFHVFYQLLSGASEELLNKLKLERDFSRYNYL-SLDSAKVNGVDDAANFR
                                                                                                                                                                                                                                                                          RVVHQNHGERNFHVFYQLLEGGEEETLRRLGLERNPQSYLYLVKGQCAKVSSINDKSDWK 266
                                                                                                                                                                                                                                                                                                                                                                RGGAVRDRLLQSNPVLEAFGNAKTLRNDNSSRFGKYMDVQFDFKGAPVGGHILSYLLEKS 206
                      RLFSWLVNRINESIKAQTKVRKK----
                                                                                              ESKIKDKMSXKKFVNCRHXSISSRRAFSFRTVEPTEKVSTTLNVAQAYYARDALAKNLYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IGVGDMVLLEPL-NEETFINNLKKRFDHSEIYTYIGSVVISVNPYRSLPIYSPEKVEEYR 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              preventing, treating or ameliorating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative 118; Mismatches 190; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32.8%; Score 1770.5; DB 2 49.9%; Pred. No. 9.2e-142;
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                      VMGVLDIYGFEIFEDNSFEQFIINYCNEKLQQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            man secreted protein a medical condition
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02-MAR-2000
16-MAR-2000
17-MAR-2000
17-MAR-2000
19-MAY-2000
07-JUN-2000
28-JUN-2000
07-JUN-2000
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07-JUN-2000
07-JUN-2000
                                                                      11-JUL-2000
14-JUL-2000
26-JUL-2000
26-JUL-2000
14-AUG-2000
14-AUG-2000
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14-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase; ligase; hyperproliferative disorder; immunodeficiency disorder; autoimmune disorder; neurological disorder; metabolic disorder; inflammatory disorder; cardiovascular disorder; reproductive disorder; blood-related disorder; infectious disorder; cytostatic; anti arthritic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU23125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nephrotropic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LYRDLSQAMWKASHALIKSLFPEGNPAKINLKRPPTAGSQFKASVATLMKNLQTKNPNYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TFLEKLEDTVKPHPHFLTH--KLADQKTRKSLDRGEFRLLHYAGEVTYSVTGFLDKNNDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LFIELTLKSEQEEYEAEGIAWEPVQYFNNKIICDLVEEKFKGIISILDEECLRPGEATDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PMWAGRPQDGVAVLVRHLGYKPEEYKMGRTKIFIRFPKTLFATED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TFLEKLNQVCATHQHFESRMSKCSRFLNDTSLPHSCFRIQHYAGKVLYQVEGFVDKNNDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IFIELTLKEEQEEYIREDIEWTHIDYFNNAIICDLIENNTNGILAMLDEECLRPGTVTDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RCIKPNDKKAAHIFNEALVCHQIRYLGLLENVRVRRAGYAFRQAYEPCLERYKMLCKQTW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
                2000US-0184664

2000US-0189874

2000US-0190076

2000US-0190076

2000US-0190123

2000US-0209467

2000US-0211647

2000US-0211647

2000US-02116480

2000US-02116480

2000US-02117496

2000US-0217496

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2000US-0226681. 2000US-0226868. 2000US-0227182. 2000US-0225757. 2000US-0225758. 2000US-0225759.

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The present invention relates to the isolation of novel human enzyme CC polypeptides, and the cDNA (AAS40785-AAS41684) and genomic sequences CC encoding them. The enzyme polypeptides of the invention may comprise the CC functional classes of oxidoreductases, transferases, hydrolases, lyases, CC isomerases or ligases. The sequences of the invention are useful in the CC diagnosis, treatment, prevention and/or prognosis of a wide range of CC disorders including hyperproliferative disorders (e.g. cancer), CC (e.g. arthritis), neurological disorders (e.g. ALZheimer's disease), CC (e.g. arthritis), neurological disorders (e.g. ALZheimer's disease), CC (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis), CC (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis), CC (e.g. infertility) and infectious disorders (e.g. Influenza). The CC polynucleotides of the invention can also be used in gene therapy. CC (aAUZ2915-AAUZ3814 represent the novel human enzyme polypeptides of the
                invention.

Note: The sequence data for this patent did not specification, but was obtained in electronic fo at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-NOV-2000)
01-DEC-2000)
05-DEC-2000)
05-DEC-2000)
05-DEC-2000)
06-DEC-2000)
06-DEC-2000)
08-DEC-2000)
                                                                                                                                                                                                                                                                                                                                                                   Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous
                                                                                                                                                                                                                                                                                                                                   Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-465566/50
N-PSDB; AAS40995.
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08-NOV-2000;
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Similarity

DB 22;

Length 1026;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KYLTRLLGVEGTTLREALTHRKIIAKGEELLSP-LNLEQAAYARDALAKAVYSRTFTWLV 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KSDWKVMRKALSVIDFTEDEVEDLLSIVASVLHLGNIHFAADEDSNAQ-----VTTENQL 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SRVVHQNHGERNFHVFYQLLEGGEEETLRRLGLERNPQSYLYLVKGQCAKV---SSI-ND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGA--VRDRLLQSNPVLEAFGNAKTLRNDNSSRFGKYMDVQFDFKGAPVGGHILSYLLEK 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RELYERPPHLYAVANAAYKAMKHRSRDTCIVISGESGAGKTEASKHIMQYIAAVTNPSQR 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GVQDFVLLENFTSEAAFIENLRRRFRENLIYTYIGPVLVSVNPYRDLQIYSRQHMERYRG 87
                                                                                                                                                                                                                                                                                ---RARLIPI--IVLLLQKAWRGTLARWR-CRRLRAIYTIMRWFR----RHKVRA----
                                                                                                                                                                                                                                                                                                                                                                           GRPQDGVAVLVRHLGYKPEEYKMGRTKIFIRFPKTLFATEDSLEVRRQSLATKIQAAWRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MCSSMNPIMAQCF----DKSELSDKKRPETVATQFKMSLLQLVEILRSKEPAYIRCIKP 609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   THHRHHLHYTSRQLC--PTDKTMEFGRDFRIKHYAGDVTYSVEGFIDKNRDFLFQDFKRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KSEQEEYEAEGIAWEPVQYFNNKIICDLVEEKFKGIISILDEECLRPGEATDLTFLEKLE 495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VSFYEVPPHLFAVADTVYRALRTERRDQAVMISGESGAGKTEATKRLLQFYAETCPAPER 147
LVVLHARGQDD
                                                                VLFSSHVRKVNR-FHKIRNRALLLTDQHLYKLDPDRQYRVMRAVPLEAVTGLSVTSGGDQ
                                                                                                                                                                                                                                           FLDHVRASFLLNLRRQLPRNVLDTSWPTPPPALREASELLRELCMKNMVWKYCRSISPEW 848
                                                                                                                                                                                                                                                                                                                                                      GSDKAAVSALLEQHGLQ-GDVAFGHSKLFIRSPRTLVTLEQS------713
                                                                                                                                                                                                                                                                                                                                                                                                                         NEDKVAGKLDENHCRHQVAYLGLLENVRVRRAGFASRQPYSRFLLRYKMTCEYTWPNHLL 672
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                               LFVLHVQREDN 967
                                                                                                                                        MPQIKAKVAAMGALQGLRQDWGCRRAWARDYLSSATDNPTASSLFAQRLKTLRDKDGFGA
                                                                                                                                                                       KQQLQQKAVASEIFKGKKDNY--PQSVPRLFISTRLGTEEISPRVLQSL-----
                                                                                                                                                                                                              HLAELQRRF
                                                                                                                                                                                                                                                                                                                  FHWRQKFLRVKRSAICIQSWWRGTLGRRKAAKRKWAAQTIRRLIRGFILRHSPRCPENAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KQEQEEYEREGITWQSVEYFNNATIVDLVERPHRGILAVLDEACSSAGTITDRIFLQTLD
                                                                                                 IQYAVPVVKYDRKGYKPRPRQLLLTPSAVVIVE---DAKVKQRIDYANLTGISVSSLSDS 956
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                                                                                                                                                                                                            -QAARQPPLYGRDLVWPLPPAVLQPFQDTCHALFCRWRARQLVKNIPPSD
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GVDDMVLLPQIT-EDAIAANLRKRFMDDYIFTYIGSVLISVNPFKQMPYFTDREIDLYQG GVQDFVLLENFTSEAAFIENLRRRFRENLIYTYIGPVLVSVNPYRDLQIYSRQHMERYRG

76 87 Matches 400;

Similarity

Conservative 152;

Mismatches

304;

Indels 193;

Gaps

23;

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RESULT 9
AAU97544
                                                         The present invention relates to a new probe comprising or consisting of CC an immobilised phosphatidyl acid derivative attached on to a solid CC support, or a phosphatidic acid (PA) incitionalised solid support. The CC probe of the invention is useful in an assay method for identifying CC and/or isolating a protein that binds to the probe. The invention is also useful for detecting, measuring, identifying and/or isolating more than CC (PIPN) from a test sample e.g. a tissue of tissue culture extract. The cassay is also useful for detecting, measuring, identifying and/or isolating protein in CC assay is also useful for detecting, measuring, identifying and/or constaining prosphatidic acid and/or phosphoinositide-binding proteins in cassay is also useful for detecting, measure the ability of an agent, applied to the probe, to detect and/or measure the ability of an agent, applied to phosphatidic acid and/or phosphoinositide-binding protein-containing contest sample, to agonise or antagonise protein-probe binding. The probe is useful for containing contest and/or measure the ability of an agent, applied to the probe, to caponise or antagonise protein-probe binding. The probe is useful for containing contest and/or antagonist or antagonist of phosphatidic acid/ phosphoinositide binding protein-probe binding. The probe is useful for containing contest and/or antagonist. The invention is also useful for identifying important proteins for signal transduction, housekeeping and diagnosis. The probe is useful as an important research tool in fundamental research containing contest the human myosin-IF protein MYOIF of the invention.
Query Match
Best Local
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(UYCA-)
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                                                         Sequence
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15-DEC-2000;
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atidic acid; signal transduction; housekeeping; myosin-1F.
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2000GB-0030637.
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31.8%;
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Score 1714.5; DB 2
Pred. No. 1.1e-136;
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                 Length
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77 88

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RESULT 10
AAUZ3128
ID AAUZ3128 standard; Protein; 909
                                                                                                                                                                                               916 PRPRQLLLTPSAVVIVEDAK-----
                                                                          GGGGTRSVTFSRGFGDLAVLKVGGRTLTV 913
                                                                                                 GGPGRDGIIDFTSGSELLITKAKNGHLAV 1036
                                                                                                                                            QREDNKQKGDVVLQSDHVIETLTKT---ALSADRVNNININQGSITFA-------
                                                                                                                                                                  PIKRDLILTPKCVYVIGREKMKKGPEKGQVCEVLKKKVDIQALRGVSLSTRQDDFFIL--
                                                                                                                    -QED------AADSFLESVFKTEFVSLLCKRFEEATRRPLPLTFSDTLQFRVKKEGW
                                                                                                                                                                                                                    EASNILLNKKERRRNSINRNFVGDYLGLEE-RPELRQFLGKKERVDFADSVTKYDRR-FK
                                                                                                                                                                                                                                    VASEIFKGKKDNYPQSVPRLEISTRLGTEEISPRVLQSLG-SEPIQYAVPVVKYDRKGYK 915
                                                                                                                                                                                                                                                                                           FLLNLRRQLPRNVLDTSWPTPPPALREASELLRELCMKNMVWKYCRSISPEWKQQLQQKA
                                                                                                                                                                                                                                                                                                                                                                                 RVKRSAICIOSWWRGTLGRRKAAKRKWAAQTIRRLIRGEILRHSPRCPENAFFLDHVRAS
                                                                                                                                                                                                                                                                                                                                                                  HLLRAVNMEDDQYQMGSTKVFVKNPESLFLLEEVRERKFDGFARTIQKAW------
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26-JUL-2000;
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28-JUN-2000;
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2000US-0230438.
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2000US-0220963

2000US-0224518

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2000US-0225266

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2000US-0199123
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2000US-0231968. 2000US-0232397. 2000US-0232398. 2000US-0232399.

14-SEP-2000; 14-SEP-2000; 14-SEP-2000; 14-SEP-2000;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of a wide range of disorders including hyperproliferative disorders (e.g. cancer), immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g. arthritis), neurological disorders (e.g. Alzheimer's disease), metabolic disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis), blood-related disorders (e.g. heamophilia), reproductive disorders (e.g. infertility) and infectious disorders (e.g. influenza). The polynucleotides of the invention can also be used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                Note: The sequence data for this patent did not form specification, but was obtained in electronic format at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to the isolation of novel human enzyme polypeptides, and the cDNA (AAS40785-AAS41684) and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous
                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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EQSHQAVTEAMRVIGFSPEEVESVHRILAAILHLGNIEFVETEEGGLQKEGLAVAEEALV
                              KSDWKVMRKALSVIDFTEDEVEDLLSIVASVLHLGNIHFAADEDSNAQ-----VTTENQL
                                                                                                                                                                                                           VSFYEVPPHLFAVADTVYRALRTERRDQAVMISGESGAGKTEATKRLLQFYAETCPAPER 147
                                                                                                                                                                                                                                                          GKPDFVLLDQVTME-DFMRNLQLRFEKGRIYTYIGEVLVSVNPYQELPLYGPEAIARYQG
                                                            RELYERPPHLYAVANAAYKAMKHRSRDTCIVISGESGAGKTEASKHIMQYIAAVTNPSQR
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2000US-0241787 2000US-0241786. 2000US-0237038. 2000US-0237039. 2000US-0237040.

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2000US-0246475. 2000US-0246474

2000US-0246524 2000US-0246523 2000US-0246478

2000US-0249245. 2000US-0249264. 2000US-0249265.

2000US-0249216. 2000US-0249217. 2000US-0249218.

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2000US-0249210. 2000US-0249211. 2000US-0249212.

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N-PSDB; ABN32444
                   WPI; 2002-292408/33
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                                                                       Xue AJ,
                                                                                           Tang YT,
                                                                                                                                   (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                                                                                                                                                            Human; antianaemic; vulnerary; antiinflammatory; immunomodu antiinfertility; cerebroprotective; cytostatic; rheumatic; neuroprotective; antiparkinsonian; protein therapy; EST;
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                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                           Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LYNSTDPTLRAMWPDGQQDITEVT--KRPLTAGTLEKNSMVALVENLASKEPEYVRCIKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MCSSMNPIMAQCF----DKSELSDKKRPETVATOFKMSLLQLVEILRSKEPAYIRCIKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                             Zhou P,
Wehrman
                                                                               Asundi V,
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                                                         Zhang J,
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Best Local Simi
Matches 378;
                   726
                             633 RWRGDEROGVQHLLRAVNMEPDQYQMGSTKVFVKNPESLFLLEEVRERKFDGFARTIQKA
                                                                                                   606 CIKPNDAKQPGREDEVLIRHQVKYLGLMENLRVRRAGFAYRKKYEAFLQRYKSLCPETWP
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                                                                                                                                                                                                                                                                                                               352 DPLVEAINRAM-QKPQEEYS-----IGVLDIYGFEIFQKNGFEQFCINFVNEKLQQIFI
                                                                                                                                                                                                                                                                                                                             372 TWLVRKINRSLASKDAESPSWRSTTVLGLLDIYGFEVFQHNSFBQFCINYCNEKLQQLFI 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention provides the protein and coding sequences of 444 (ESTs). They can be used to stimulate cell growth, to regulate e.g. in burn treatment, to regulate the immune system e.g. to treat aplastic anaemia, to help tissue regrowth multiple sclerosis, to regulate activin or inhibin e.g. to treat infertility, to regulate haemostasis or thrombolysis e.g. to treat stroke and cancer, to screen for drugs, to treat inflammatory conditions e.g. rheumatoid arthritis, and to treat nervous system disorders e.g. Parkinson's disease. The present sequence is a protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                      292 LAFPAYLLGIDSGRLQEKLTSRKMDSRWGGRSESINVTLNVEQAAYTRDALAKGLYARLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     An isolated polynucleotide for treating diseases associated with encoded polypeptide such as cancer and multiple sclerosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2;
WRGFHWROKFLRVKRSAICIQSWWRGTLGRRKAAKRKWAAQTIRRLIRGFILRHSPRCPE 785
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70 PYRDLQIYSRQHMERYRGVSFYEVPPHLFAVADTVYRALRTERRDQAVMISGESGAGKTE 129
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                                                                                   CIKPNETKRPRDWEENRVKHQVEYLGLKENIRVRRAGFAYRRQFAKFLQRYAILTPETWP
                                                                                                                                                           LFRNLKETMCSSMNPIMAQCFDKSELSDKK-RPETVATQFKMSLLQLVEILRSKEPAYIR
                                                                                                                                                                                                DQTLLQKLQAAVGTHEHF------NSWSAG-FVIHHYAGKVSYDVSGFCERNRDV 512
                                                        MWAGRPODGVAVLVRHLGYKPEEYKMGRTKIFIRFPKTLFATEDSLEVRRQSLATKIQAA
                                                                                                                                          LFSDLIELMQSSDQAFLRMLFPEKLDGDKKGRÞSTAGSKIKKQANDLVATLMRCTÞHYIR
                                                                                                                                                                                                                                                       DLTFLEKLEDTVKPHPHFLTHKLADQKTRKSLDRGEFRLLHYAGEVTYSVTGFLDKNNDL 546
                                                                                                                                                                                                                                                                                                                                                                                       DGTDDRSDFGETLSAMQVIGISIQQL--VLQLVAGILHLGNISFC--EDGNYARVESVDL
                                                                                                                                                                                                                                                                                                                                                                                                                                              GGEPDGGKISNFLLEKSRVVMQNENERNFHIYYQVQGRAGGEGAPPGAQRGGQWEGKHLG 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GHGRADEGSQGLSQASTRCMNMATPSSWLEGASQEQRQNLGL-MTPDYYYYLNQSDTYQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATKRLLQFYAETCPAPERGGAVRDRLLQSNPVLEAFGNAKTLRNDNSSRFGKYMDVQFDF 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAKYIMGYISKYSGGGEKVQHYKDIILQSNPLLEAFGNAKTVRNNNSSRFGKYFEIQESR 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1089 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29.0%; Score 1565; DB 23; 35.7%; Pred. No. 6.3e-124; tive 147; Mismatches 283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels 252;
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity.
                                                                                                                                                                                                                                                      New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                              biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                  31-MAR-2000;
23-AUG-2000;
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)B; AAS84797.
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2000US-0649167
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                                                                                                                                                                                                                                                                                                                                                                      Liu C,
                                                                                                                                                                                                            ID No 50969; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --EASNILLNKKERRRNSINRNFVGDYLGLEE-RPELRQFLGKKERVDFAD
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Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                  PHPHFLTHK-----LADQKTRKSLDRG-EFRLLHYAGEVTYSVTGFLDKNNDLLFRNLK 552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AEVERVKDVLLKSTCVLEAFGNARTNRNHNSSRFGKYMDINFDFKGDPIGGHIHSYLLEK 188
                                                                                                                  GFHWRQKFLRVKRSAICIQSWWRGTLGRRKAAKRKWAAQTIRRLIRGFILRHSPRCPENA
                                                                                                                                                                                                                                                               KPNDAKQPGRFDEVLIRHQVKYLGLMENLRVRRAGFAYRRKYEAFLQRYKSLCPETWPMW
                                                                                                                                                                                                                                                                                                 RMLYNSTDPTLRAMWPDGQQDITEVT--KRPLTAGTLFKNSMVALVENLASKEPFYVRCI
                                                                                                                                                                                                                                                                                                                                                               HHLHYTSRQVPPAVPVPPQWADKTMEFGRDFRIKHYAGD-----
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WKQQLQQKAVASEIFKGKKDNY 869
                                                               FFLDHVRASFLLNLRRQLPRNVLDTSWPTPPPALREASELLRELCMKNMVWKYCRSISPE
                                                                                                                                                                 ALKEQHGL-----QGDVAFGHSKLFIRSPRTLVTLEQS----
                                                                                                                                                                                               AGRPQDGVAVLVRHLGYKPEEYKMGRTKIFIRFPKTLFATEDSLEVRRQSLATKIQAAWR
                                                                                                                                                                                                                                KPNEDKVAGKLDENHCRHQVAYLGLLENAAVS--
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Pred. No. 3.7e-111;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        capable of detecting 1000 or more genes from Drosophila. The invent useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                        specification, at ftp.winc in
                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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| 723 DMPQIKAKVAAMGALQGLRQDW
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      TYTGSILVAVNPYQILPIYTGDQIKLYKERKIGELPPHIFAIGDNAYAHMKRYRQDQCIV
                                                                                        ISGESGAGKTEATKRILLOFYAETCPAPERGGAVRDRLLOSNPVLEAFGNAKTLRNDNSSR
                                                               ISGESGAGKTESTKLILQYLA---AISGKHSWIEQQILEANPILEAFGNAKTIRNDNSSR
                                                                                                                                                                              TYIGPVLVSVNPYRDLQIYSRQHMERYRGVSFYEVPPHLFAVADTVYRALRTERRDQAVM 118
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2000US-0614150
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                                                                             SLEVRRQSLATK----IQAAWRGFHWRQKFLRVKRSAICIQSWWRGTLGRRKAAKRKWAA
                                                                                                           EFVERYRFLIPGVPPAHRTDCQAATSRICAVVLG--KSDYQLGHTKVFLKDAHDLF----
                                                                                                                                 AFLQRYKSLCPETWPMWAGRPQDGVA-VLVRHLGYKPEEYKMGRTKIFIRFPKTLFATED | : : | | :|::| | |::: | | |
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                                                -LEQERDRVLTRKILILQRSIRGWYYRRRFLRLRAAAITVQRFWKGYAQRKRYRNMRVGY
                                                                                                                                                                                                  QLVEILRSKEPAYIRCIKPNDAKQPGREDEVLIRHQVKYLGLMENLRVRRAGFAYRRKYE
                                                                                                                                                                                                                                                               YSVTGFLDKNNDLLFRNLKETMCSSMNPIMAQCFDKS---ELSDKKRPETVATQFKMSLL 590
                                                                                                                                                                                                                                YDTRGFLDKNRDTFSPDLLHLVSQSTNKFLRQIFAQDIEMGAETRKRTPTLSTQFRKSLD
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AAB42651

AAB42651 standard; Protein; 512

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U8-FEB-2001 (first entry)

Human ORFX ORF2415 polypeptide sequence SEQ ID NO:4830.

Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatologica; immunosuppressive; antiantamnatory; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antiinflammatory disease; coagulation; thrombosis; contraceptive.

S Homo sapiens

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nucleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders, osteoarthritis, graft vs host disease, cardiovascular disease, diabetes mellitus, hypertension, hypothyroidism, cholesterol ester storage, systemic luperythematosus, severe combined immunodeficiency (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune disorders, asthma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an OREX-associated disorder. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-MAR-1999; 99US-0127607
02-APR-1999; 99US-0127636
05-APR-1999; 99US-0127728
30-MAR-2000; 2000US-0540763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11; Page 4015-4016; 5507pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000-602362/57
                                                                                                                                                                                                                                                                                                                                            TGIDQSVLERAFSFRTVEAKQEKVSTTLNVAQAYYARDALAKNLYSRLFSWLVNRINESI
                                   LGVEGTTLREALTHRKIIAKGEELLSPLNLEQAAYARDALAKAVYSRTFTWLVRKINRSL
                                                                           TVRNAMQIVGFMDHEAESVLAVVAAVLKLGNIEFKPESRVNGLDESKIKDKNELKEICEL
                                                                                                               VMRKALSVIDFTEDEVEDLLSIVASVLHLGNIHFAADEDSN----AQVTTENQLKYLTRL 322
                                                                                                                                                         RVVKQPRGERNFHVFYQLLSGASEELLNKLKLERDFSRYNYL-SLDSAKVNGVDDAANFR
                                                                                                                                                                                               RVVHQNHGERNFHVFYQLLEGGEEETLRRLGLERNPQSYLYLVKGQCAKVSSINDKSDWK
                                                                                                                                                                                                                                         EVNQVKEQLLQSNPVLEAFGNAKTVRNDNSSRFGKYMDIEFDFKGDPLGGVISNYLLEKS
                                                                                                                                                                                                                                                          RGGAVRDRLLQSNPVLEAFGNAKTLRNDNSSRFGKYMDVQFDFKGAPVGGHILSYLLEKS 206
                                                                                                                                                                                                                                                                                                                       NRNFYELSPHIFALSDEAYRSLRDQDKDQCILITGESGAGKTEASKLVMSYVAAVCGKGA 133
                                                                                                                                                                                                                                                                                                                                                                                                         IGVGDMVLLEPL-NEETFINNLKKRFDHSEIYTYIGSVVISVNPYRSLPIYSPEKVEEYR 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         260;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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RESULT 15
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Best Local
                                                                                                                                                                                                     capable of detecting 1000 or more genes from Drosophila. The inventuaseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA discloses genomic DNA sequences (ABL16176-ABL30511).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster polypeptide SEQ ID NO 15276
                                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                    New isolated nucleic acid genes from Drosophila and interactions -
                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB;
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                                                                                                           Sequence
                                                                                                                                    at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                   specification, but was obtained in electronic
                                                                                                                                                              The sequence data for this patent did not form
                                                                                                                                                                              sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 15276; 21pp + Sequence Listing; English
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N-PSDB; ABL06931.
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11-JUL-2000;
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                  EEISPRVLQSLGSEPIQYAVPVVKYDRKGYKPRPRQLLLTPSAVVIV 931
                                      EELLR-----EREQREQQEKRLQEEQRLKA
                                                         SELLRELCMKNMVWKYCRSISPEWKQQLQQKAVASEIFKGKKDNYPQSVPRLFISTRLGT 884
                                                                                                -----LIRGFILRHSPRCPENAFFLDHVRASFLLNLRRQLPRNVLDTSWPTPPPALREA
                                                                                                                     RVLFRRYMKRYREAIITVQRYWRGRLQRRKYQVMRQGFHRLGACIAAQQLTTKFTMVRCR
                                                                                                                                     LARQICEVALPADSDRQYGKTKLFLR-----DEDDASLELQRSQLMLKSIVTIQRGIR 758
                                                                                                                                                                           LVRHLGY----KPEEYKMGRTKIFIRFPKTLFATED--SLEVRRQSLATK----IQAAWR 727
                                                                                                                                                                                                                                                             NPIMAQCFDKSELSD--KKRPETVATQFKMSLLQLVEILRSKEPAYIRCIKPNDAKQPGR 617
                                                                                                                                                                                                                                                                                                                                 EHINWQHIEFQDNQQILDLIGMKPMNLMSLIDEESKFP-KGTDQTLLEKLH------
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Qy 281 EVEDILSIVASVLHLGNIHFAADE-DSNAQVTTENQLKYLTRLLGVEGTTLREALTHR    1	Db 167 TDRENQSILITGESGAGKTVNTKRVIQYFASIAAIGDRGKKDNANANKGTLEDQIIQANP Qy 161 VLEAFGNAKTLRNDNSSRFGKYMDVQFDFKGAPVGGHILSYLLEKSRVVHQNHGERNFHV	4 48 50 107 110	Ouery Match 22.1%; Score 1191; DB 4; Length 1939; Best Local Similarity 35.6%; Pred. No. 5.3e-104; Matches 281; Conservative 142; Mismatches 303; Indels 64;	RESULT 1  US-09-310-187A-1  Sequence 1, Application US/09310187A  Patent No. 6358751  GENERAL INFORMATION:  APPLICANT: Benichou, Gilles  APPLICANT: Benichou, Gilles  TITLE OF INVENTION: Involvement of Autoantigens in Cardiac  TITLE OF INVENTION: Graft Rejection  FILE REFERENCE: UCSF-090  CURRENT APPLICATION NUMBER: US/09/310,187A  CURRENT APPLICATION NUMBER: US/09/310,187A  CURRENT APPLICATION SER US/09/310,187A  COURTAGE: FastSEQ for Windows Version 4.0  SEQ ID NO 1  LENGTH: 1939  TYPE: PRT  GORGANISM: Homo Sapiens	ALIGNMENTS	28 120.5 2.2 874 3 US-08-804-439A-15 29 120.5 2.2 874 3 US-08-720-229-15 30 120 2.2 2154 2 US-08-814-349-4 31 117.5 2.2 1151 4 US-09-134-0006-3242 Sequence 32 115 2.1 1200 3 US-08-840-006-5 34 112 2.1 1200 3 US-08-840-006-6 34 112 2.1 1181 2 US-08-840-006-6 35 111.5 2.1 1181 2 US-08-48-940-2 36 111 2.1 1181 2 US-08-48-940-2 37 111 2.1 1066 4 US-09-541-782-8 Sequence 38 111 2.1 1066 4 US-09-541-782-8 Sequence 39 111 2.1 1066 4 US-09-541-782-8 Sequence 40 110 2.0 787 1 US-08-78-73-2 40 110 2.0 787 1 US-08-73-462-8 Sequence 41 108 2.0 805 3 US-08-915-213-4 42 108 2.0 805 3 US-08-915-213-4 43 108 2.0 805 5 PCT-US96-10251-4 Sequence 44 108 2.0 805 5 PCT-US96-10251-4 Sequence 45 108 2.0 1280 2 US-08-583-276-19
HRKI 339	PANP 226  WHY 220  WHI 286  WHI 286  TED 280      :	4 4 4 4	Gaps 18			e 15, Applice 17, Applice 3,42, Applice 5, Applice 7, Applice 6, Applice 7, Applice 7, Applice 8, Applice 8, Applice 8, Applice 8, Applice 8, Applice 9, A

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RESULT 2
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                                                                                                                                                                   NAME/KEY: MOD_RES
LOCATION: (143)
OTHER INFORMATION:
NAME/KEY: MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: A METHOD FOR THE DIRECT DIAGNOSTIC DETECTION OF TITLE OF INVENTION: GENETICALLY CAUSED PATHOGENIC POINT MUTATIONS FILE REFERENCE: 10496/P63231US0
CURRENT APPLICATION NUMBER: US/09/147,404
CURRENT FILING DATE: 1999-04-06
CURRENT FILING DATE: 1999-04-06
CURBER OF SEQ ID NOS: 3
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                                               LOCATION: (403)
OTHER INFORMATION:
                  NAME/KEY: MOD_RES
LOCATION: (453)
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OTHER INFORMATION:
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OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                               PatentIn
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NIER, VOLKER
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NAME/KEY: MOD_RES
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US-09-172-422-1
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                                                                                                                                                                                                                                                                                                                                                                GENERAL
                                                                   SEQ ID NO 1
                                                                                                                                                      APPLICANT: Adams, Arwen E.
APPLICANT: Chiu, Choi Ying
APPLICANT: Duhl, David
APPLICANT: Duhl, David
APPLICANT: Gorman, Susan W.
APPLICANT: Gorman, Susan W.
APPLICANT: Sheffield, Val
APPLICANT: Welch, Juliet
TITLE OF INVENTION: MYOSIN IXA AND CYCLIC NUCLEOTIDE GATED
TITLE OF INVENTION: COMPOSITIONS, METHODS, AND USES THEREOF
TITLE OF INVENTION: COMPOSITIONS, METHODS, AND USES THEREOF
TITLE OF INVENTION: COMPOSITIONS, METHODS, AND USES THEREOF
                                                                                                                        CURRENT APPLICATION NUMBER: US/09/172,422A CURRENT FILING DATE: 1998-10-14
                                                                                    NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
           LENGTH: 2548
TYPE: PRT
ORGANISM: Homo sapien
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Best Local Similarity
Matches 320; Conserv
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                                                                                                                                                                                                                                                     DAKQPGRFDEVLIRHQVKYLGLMENLRVRRAGFAYRRKYEAFLQRYKSLCPETWPMWAGR 670
                                                                                                                                                                                                                                                                                               NSLKHLTRLTLQDRITKSLLHLHKKKKPPSISAQFQASLSKLMETLGQAEPYFVKCIRSN 919
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YHVFYYLLAGASEDERSAFHL-KQPEEYHYLNQITKKPLRQSWDDYCYDSEPDCFTVEGE 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FHVFYQLLEGGEEETLRRLGLERNPQSYLYL------VKGQCAKVSSI 259
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                                                              RVKRSAICIQSWWRGTLGRRKAA----KRKWAA-----QTIRRLI-----RGFILR 778
                                                                                               RQHFLHLRQASVIIQRFWRNYLNQKQVRDAAVQKDAFVMASAAALLQASWRAHLERQRYL 1095
                                                                                                                                   TEDSLEVRRQSL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                   SMDSFSFLQHPVHQRSLEILQRCKEEKYSITRKNPRTPLSDLQGMNALNEKNQHDTFDIA 799
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                                                                                                                                                                                                                                  AEKLPLRFSDVLVLRQLRYTGMLETVQIRQSGYSSKYSFQDFVSHFHVLLPRNIIPSKFN
                                                                                                                                                                 IQD----FFRKINLNPDNYQVGKTMVFLKEQERQHLQDLLHQEVLRRIILLQRWFRVLLC 1035
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-PENAFFLDHVRASFLLNLRRQLPRNVLDTSWPTPPPALREASELL 828
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25.2%; Pred. No. 1.4e
Live 205; Mismatches
                                                                                                                                                                                                                                                                                                                              ---KKRPETVATQFKMSLLQLVEILRSKEPAYIRCIKPN 610
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1.4e-95;
                                                                                                                                 -----ATKIQAAWRGFHWRQKFL 736
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CLASSIFICATION:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Grook, Wannell M.
REGISTRATION NUMBER: 31 071
REFERENCE/DOCKET NUMBER: 3595-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEPHONE: (303) 863-0223
TO NO: 3:
                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1886 smino acids
TYPE: amino acids
                                                                                                                                                                                           Matches
                                                                                                                                                                                                             Query Match
Best Local
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US-08-938-105-3
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GENERAL INFORMATION:
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                                                 106 ERVAAWHIYTYSGLFCVTVNPYKWLPVYNAEVVAAYRGKKRSEAPPHIFSISDNAYQYML
                      110 TERRDQAVMISGESGAGKTEATKRLLQFYAETCPAPERG-----
                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                   50
                                                                                                                                  47
                                                                                                                                                                                Local Similarity 32.1%; pr
nes 253; Conservative 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross p.C.
STREET: 1700 Lincoln St., Sui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Leinwand, Leslie A.
APPLICANT: Vikstrom, Karen L.
TITLE OF INVENTION: TRANSGENIC MODEL FOR HEART FAILURE
                                                                                                                                     4 RASALGSDGVRVTME-----SALTARDRV------GVODFVLLENETSEAAFIENLR 49
                                                                                                                                                                                                                                                                                  TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Denver
STATE: CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1214 ESNRISRESSYDCLKESPNKQQERAQSQSGVDL---QED-----VLVRER------
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                                                                           RRERENLIYTYIGPVLVSVNPYRDLQIYSROHMERYRGVSTYEVPPHLFAVADTVYRALR 109
                                                                                                          KAKIVSREGGKVTAETENGKTVTVKEDQVMQQNPPKFDKIEDMAML-TFLHEBAVLYNLK 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             949 SVSSLSDSLEVLHVOREDNKOKGDVV---LQSDH-----VIETLTKTALSADRVN 995
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                                                                                                                                                                                                                                                                protein
                                                                                                                                                                         18.9%; Score 1018; DB 4; 32.1%; Pred. No. 1.8e-87; valive 136; Mismatches 286;
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                                                                                                                                                                                                       Length 1886;
                   ---GAVRDRLLQSNP 160
                                                                                                                                                                        Indels 114;
                                                                                                                                                                     Gaps
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                                                                                                                                                                     17;
                                                                                                                                                                                                                                                                                                                                                       US-09-012-515A-12
      COUNTRY: USA
ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                    Sequence 12, Application US/09012515A
Patent No. 6127521
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                                                                                                                                                                                                          APPLICANT: Berlin, Vivian
APPLICANT: Chiu, Maria Isabel
APPLICANT: Cottarel, Guillaume
APPLICANT: Damagnez, Veronique
TITLE OF INVENTION: IMMUNOSUPPRE:
NUMBER OF SEQUENCES: 35
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                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT
STREET: One Post Office Square
                                                                                                                            STATE: 1
                                                                                                                                                       CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                757 RDALLVIQW 765
                                                                                                                                                                                                                                                                                                                                                                                                                                               740 RSAICIQSW 748
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: APV-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEPAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1809 amino acids
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Best Local S
Matches 193
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FILING DATE: 20-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: VINCENT, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: ADV-036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
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753 LGRRKAAKRKWAAQTIRRLIRGFILRHSPRCPENA-FFLDHVRASFLLNLRRQLPRNVLD 811
                                                                                                                                                                                                          778 AAAWGLGQWDSMEEYTCMIPRDTHDGAFYRAVLALHQDLFSLAQQCIDKARDLLDAELTA 837
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                                                                                                                                                                                                                                                                                                                                                                                                                       501 HPHFL-----THKLADQKTRKSLDRGEFRLLHYAGEVTYSVTGF---------
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Local Similarity 19.1%; Pred. No. 2e-05;
hes 193; Conservative 121; Mismatches 318; Indels 37
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                                                                                                                              MAGESYSRAYGAMVS----C----
                                                                                                                                                                   RAGFAYRRKYEAFLQRYKSLCPETWPMWAGRPQDGVAVLVRHLGYKPEE---YKMGRTKI 696
                                                                                                                                                                                                                                                  LQLVEILRSKEPAYIRCIKPNDAKQPGRFDEVLIRHQ------VKYLGLMENLRVR 639
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                                           -----VPERREIIRQIWWERLQGCQRIVEDWQKILMVRSLVVSPHEDMRTW----
                                                                                  FIRFPKTLFATEDSLEVRRQSLATKIQAAWRGFHWRQKFLRVKRSAIC----IQSWWRGT 752
                                                                                                                                                                                                                                                                                             KMDTNKD-----DPELMLGRMRCLEALGEWGQLHQQCCEKWTLVN---DETQAKMARMAA
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amino acid

OGY: linear
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92	FQLGKKYQIFIPMVNKVLVRHRINHQRYDVLICRIVKGYTLADEEEDPLIY 49	442	Db
222	GERNFHVFY	178	Qy
177	FYAETCPAPERGGAVRDRLLQSNPVLEAFGNAKTLRNDNSS 177	137 382	Оy
s 46;	re 160; DB 4; Length 1809; d. No. 2e-05; Mismatches 318; Indels 376; Ga	Query Ma Best Loo Matches	
	Y: li TYPE: -12	TOI MOLE( -08-360	us;
	LENGTH: 1809 amino acids TYPE: amino acid		
	CHA Fo	INFORMATION SEQUENCE	
	ICATION INFORMATION: E: 617-832-1000	TELEC	
	NAME: Vincent, Matthew P. REGISTRATION NUMBER: 36,709 REFERENCE/DOCKET NUMBER: APV-036.02	REGI: REFE	·· ·· ··
	CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION:	ATTO	٠. ٠.
	APPLICATION NUMBER: US/08/360,144A FILING DATE: 20-DEC-1994	API FII	
	SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:	CURRI	٠. ٠.
	BM PC compatible STEM: PC-DOS/M	OPI CO	
	COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk	COMP	
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	oston MA	CI:	٠. ٠.
	ADDRESSEE: FOLEY, HOAG & ELIOT LLP STREET: One Post Office Square	ADI STI	·· ··
		CORRI	٠. ٠.
	Ħ.	TITLE OF	
	Cottarel,	APPL	
	ANT:	APPL	
	INFOF	Sequence Patent No GENERAL	· · · ·
	44A-12	RESULT 6 US-08-360	RES US:
	KTLLMYTVPAVQGFFRSISLSRG	1113	Db
	VVLQSDHVIETLTKTALSADRVNNI 997	973	Qy
1112	WAVMNFEAVLHYKHQNQARDEKKKLRHASGANITNATTAATTTAATATTTASTEGSNSESE 1	1053	DЬ
972		920	Qy
1052	: :	999	Db
19	GKKDNYPQSVPRLFISTRLGTEEISPRVLQSLGSEPIQYAVPVVKYDRKGYKPRPR 919	864	Qy
96	HPLPTVHPQVTYAYMKNM-WKSARKIDAFQHMQHFVQTMQQQAQHAIATEDQQ 998	947	Db
63	TSWPTPPPALREASELLRELCMKNWWKYCRSISPEWKQQLQQKAVASEIFK 86	812	Qy
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Qy	REFERENCE: APBI-P05-036	, FILE
ממ	lagnez, V.	TITLE
Qy	Chlu, I. Cottarel,	APPLI
Db	** 127	APPL
Qy	Sequence 12, Application US/09012504A Patent No. 6464974	; Sequent
Db	7 12-504A-12	RESULT US-09-0
Qy	1160	
рь	1113 AESTENSPIDSPIDSRIVER CONTROL STATEMENT 997	Db 11
Qy	- 5	0у 9
Дb	1053 WAVMNFEAVLIHYKHONOARDEKKKI BUAGGALTERI : : : : : : : : : : : : : : : : : : :	Db 10
Qy	920 QLLLTPSAVVIVEDAKUKOR-TOVANITTICIONE	Qy
ДD	999 HKQELH-KLMARCFLKLGEWOLNIOGTUNGSTI	DЬ
Qy	864 GKKDNYPQSVPRLEISTRIGTEET SPEUT GG. 2-2	Qy
Db	947 HPLPTVHPQVTYAYMKNN-WKCABUTATATATATATATATATATATATATATATATATATAT	DЬ
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Qy V	640 RAGEAYRRKYEAFLORYKSLCPETWPMWAGRPODGVAVLVENICOURS	Qy
Db	778 AAAWGLGQWDSMEEYTCMIPRDTHDGAFYRAVIALHODIESI ACCOLL     ::	дь
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<del>-</del>	TVLIGEBAAKGDAKKE	дЬ
	452 VQYFNNKIICDLVEEKFKGTTSTIDE	Qy
	569 AYNPMARDLENAAFVSCWSELNEDOODELIBETER	DЬ
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	341 AKGEELLSPLNLEQAAYARDALAKAYYSRTETWI VARTARRAN SALAKAYYSRTETWI VARTARRAN SALAKAYYSTI VARTARRAN SALAKAY SALAKAYYSTI VARTARRAN SALAKAYYSTI VARTARRAN SALAKAY S	Qy
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	281 EVEDLLSTVASVLHLGNIHFAADEDSNAOVTTENOTUVITEN	Qy
	493 QHRMLRSGQGDALASGPVETGPMKKIH	Дb
-	223 QLLEGGEEETLRRLGLERNPOSYLYI VECOGNETION	νο

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CURRENT FILING DATE: 1998-01-23
PRIOR APPLICATION NUMBER: 08/360,144
PRIOR FILING DATE: 1994-12-20
PRIOR APPLICATION NUMBER: 08/250,795
PRIOR FILING DATE: 1994-05-27
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin version 3.1
LENGTH: 1809
TYPE: PRT
ODGANICM: Mammalian
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947 HPLPTVHPQVTYA------YMKNN-WKSARKIDAFQHMOHFVOTMQQQAQHATATEDQQ 998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 3.0%; Score 160; DB 4; Length 1809; Best Local Similarity 19.1%; Pred. No. 2e-05; Matches 193; Conservative 121; Mismatches 318; Indels 376;
                                      812 TSWPTPPPALREASELLRELCMKNWVWKYCRSISP-----EWKOQLQQKAVASEIFK 863
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                                                                                                                  LGRRKAAKRKWAAQTIRRLIRGFILRHSPRCPENA-FFLDHVRASFLLNLRRQLPRNVLD 811
                                                                                                                                                          -----VPERRETIRQIWWERLOGCORIVEDWOKILMVRSLVVSPHEDMRTW----
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                                                                              -----LKYASLCGKSGRLALAHKTLVLLLGVD----PSRQLD
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; LENGTH: 2549 amino
; TYPE: amino acid
; STRANDEDNESS: sing
; TOPOLOGY: linear
; MOLECULE TYPE: pepti
US-08-471-112A-3
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                                      Query Match 3.0%; Score 160; DB 4; Length 2549; Best Local Similarity 19.1%; Pred. No. 3.7e-05; Matches 193; Conservative 121; Mismatches 318; Indels 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRAL
ZIP: 20005-331,
COMPUTER READABLE FORM:
MEDDIUM TYPE: Floppy disk
MEDDIUM TYPE: IBM PC compatible
TWOTER: IBM PC compatible
TWOTEN: PC-DOS/MS-DOS
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                          NAME: Siekman, Michael T.
REGISTRATION NUMBER: 36,276
REFERENCE/DOCKET NUMBER: 01142.0058-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/384,524
FILING DATE: 13-FEB-1995
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US OF FILING DATE: 08-MAR-1994 ATTORNEY/AGENT INFORMATION: NAME: Siekman, Michael T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 08/312,023 FILING DATE: 26-SEP-1995 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1053 WAVMNFEAVLHYKHQNQARDEKKKLRHASGANITNATTAATTAATATTTASTEGSNSESE 1112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              973
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     999 HKQELH-KLMARCFL--KLGEWQLN---LQGINESTIPKVLQYYSAATEHDRSWYKAWHA 1052
137 FYAETCPAPERGGAVR--DRLLQS-----NPVLEAFGNAKTLRN---DNSS--- 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  864 GKKDNYPQSVPRLFISTRLGTEEISPRVLQSLGSEPI----QYAVPVVKYDRKGYKPRPR 919
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CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Finnegan, Henderson, Farabow, Garrett ADDRESSEE: Dunner, L.L.P. STREET: 1300 I Street, N.W.
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Nakanishi, Koji
Chen, Yanqiu
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                                      Gaps
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QLVEILRSKEPAYIRCIKPNDAKQPGREDEVLIRHQVKYLGLMENLRVR  AAAMGLGQWDSMEEYTCMIPRDTHDGAFYRAVLALHQDLFSLAQQCIDKARDLLDAELTA RAGFAYRKYEAFLQRYKSLCPETWPMWAGRPQDGVAVLVRHLGYKPEEYKMGRTKI    :        :        :
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RESULT 9
PCT-US95-06722-12
; Sequence 12, Application PC/TUS9506722
; GENERAL INFORMATION:

APPLICANT:

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APPLICATION NUMBER: US 08/250,795
FILING DATE: 27-MAY-1994
PRIOR APPLICATION NUMBER: US 08/250,795
FILING DATE: 20-DEC-1994
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 2549 amino acids
TYPE: amino acids
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 3.0%; Score 160; DB 5; Length 2549; Best Local Similarity 19.1%; Pred. No. 3.7e-05; Matches 193; Conservative 121; Mismatches 318; Indels 376; Gaps
1518 AAAWGLGQWDSNEEYTCMIPRDTHDGAFYRAVLALHODLFSLAQQCIDKARDLLDAELTA 1577
                                                                                                                                      1466 KMDTNKD-----DPELMLGRWRCLEALGEWGQLHQQCCEKWTLVN---DETQAKNARMAA 1517
                                                                                                                                                                                                       1409 TPATLESLISTNNKL--QQPEAAAGVLEYAMKHF-GELETQATWYEKLHEWEDALVAYDK 1465
                             640 RAGFAYRRKYEAFLORYKSLCPETWPMWAGRPODGVAVLVRHLGYKPEE----YKMGRTKI 696
                                                                                                   590 LQLVEILRSKEPAYIRCIKPNDAKQPGRFDEVLIRHQ-----VKYLGLMENLRVR 639
                                                                                                                                                                                                                                                                           1354 TOTLLN--LAEFMEHSDKÖPLPLRDDNGIVLLGERAAKCRAYAKA---LHYKELEFQKGP 1408
                                                                                                                                                                                                                                                                                                                                              1309 AYNPMARDLE-----NAAFVSCWSELNEDQODELIRSIELALTSQD-----IA-EV 1353
                                                                                                                                                                                                                                                                                                                                                                                                                 1288 -- SLELL------KDSSSPSLKSCWALAQ 1308
                                                                                                                                                                      540 -LDKNNDLLERNLKETMCSSMNPIMA------OCFDKSELSDKKRPETVATQFKMSL 589
                                                                                                                                                                                                                              1233 QHRMLRSGQGDALASGPVETGPMKKLH------VSTINLQKAWGAARR------ 1274
                                                                                                                                                                                                                                                                                                 452 VQYFNNKIICDLVEEKFKGIISILDE------ECLRPGEATDLTELEKLEDTVKP 500
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NUMBER OF SEQUENCES: 25
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: ASCII (text)
CURRENT APPLICATION DATA:
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F 4-	Application US/08905223 522029 50 Application US/08905223 50 Edwards, Jean-Baptiste D. 51 Duelert, Aymeric 51 Lacroix, Bruno 51 INVENTION: 55 ESTS FOR SECRETED 52 EDELENCES: 50 52 DENCE ADDRESS: 51 EST KNOBBES, Martens Olson The	793 WAVMNEEAVLHYK 973 VVLQSD 853 AESTENSPTPSPL	1687 HPLPTVHPQVTYA	7 697 1608 753 1654 812

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US-09-134-001C-3945
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APPLICANT: LYNN DOUCETEC-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDDERWIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
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PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3945, Application US/09134001C Patent No. 6380370
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PDQFDQAVVLNQLRYSGMLETVRIRKAGYAVRRPFQDFYKRYK--
                                                                                                                                                                                                                                                                                                                                                                                        -LRNDNSSRFGKYMDVQFDFKGAPVGGHILSYLLEKSRVVHQNHGERNF------HVFYQ 223
                                                                                                                                                                                                                                                                                                                                                            WLRSDQIK--GLYLDLQNEAYQSKLG-----LVHSRFSTNTFPSWKRAHPNRM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DACGIGFYANMDNKRSHDIIEKSLEMLRRLDHRGGVGADGITGDGAGIMTEIPY---QLF 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131;
                                                             DIYGFEVFQHNSFEQFCINYCN-EKLQQLFIELTLKSEQEEYEAEGIAWEPVQY-----
                                                                                                         AMLLIP---EPWLYNESNDKKVRSFY-EFYSYLME
                                                                                                                                              EELLSPLNLEQAAY--ARDALAKAVYSRTFTWLVRKINRSLASKDAESPSWRSTTVLGLL 401
                                                                                                                                                                                                                               DLLSIVASVLHLGNIHFAADEDSNAQVTTENQLKYLTRLLGVEGTTLREALTHRKIIAKG
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                                                                                                                                                                                       2.8%;
nl Similarity 29.2%;
35; Conserva+:
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                        -ISFCNGDKIGAL----
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Pred. No. 7.1e-07;
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                                                                                                                                                                                                                                                                           ---INTIKGNVNWMRARQNKLVETLFEDEKD
                        ----TDRNGL--RPGRYTITKDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
US-09-134-001C-3762
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APPLICANT: Lynn Doucette-Stamm et al
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCC
TITLE OF INVENTION: EPIDERWIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3762
LENGTH: 567
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3762, Application US/09134001C Patent No. 6380370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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PRIOR ETLING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          403
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       244 --SYLYLVKGQCAKVSSINDKSDWKVMRKALSVIDFTEDEVEDLLSIVASVLHLGNIHFA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                500 -PHPHFLTHKLADQKTRKSLDRGEFRLLHYAGEVTYSVTGFLDKNNDLLFRNLK------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            204 EKSRVVHQNHGERNF------HVFYQLLEGGEEETLRRLGLERNPQ-------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----PPIDA----YREKIVTSELSYLGSEGNL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LPYEQW----LKDYKNKNDLDN-----IYYQSS------DWDDQTLFRLQKQFAYTK 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FIVFSSEVGVIDVPEENVAFKG---
                                                                                                                                                                                     LVEEK--FKGIISILDEECLRPGEATDLTFLEKLEDTVKPHPHFLTHKLADQKTRKSLDR
                                                                                                                                                                                                                                                       QF-----CINYCNEKLQQLFIELTLKSEQEEYEAEGIAWEPV--QYFNNKIICD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       YIRCIKPNDAKQPGREDEVLIRHQVKYLGLMENLRVRRAGEAYRRKYEAFLQRYKSLCPE
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                   SELSDKKRPETVATQFKMSLLQLVEILRSKEPAYIRCIKPNDAKQPGRFDEVLIRHQVKY 629
                                                                                                    GEFRLLHYAGEVTYSVTGFLD-----KNNDL---LFRN--LKETMCSSMNPIMAQCFDK 569
                                                                                                                                              LTKSKKNLQGMVVVLH------DITNLQKLENLRREFVANVSHELKTPIT-----
                                                                                                                                                                                                                               QVFNPDQMVENKSYIGFIDDSIEKLIIE-SFRTEKVIYEQLEVAINNVHTKYFDVSCIPI
                                                                                                                                                                                                                                                                                                                -TRALFYTT-NDLARRLOKLNNSQKIQSNRLKTTLENIPSSVL-MIDKHGEIVVANHAYY 259
                                                                                                                                                                                                                                                                                                                                                       LAKAVYSRTFTWLVRKINRSLASKDAESPSWRST----TVLGLLDIYGFEVFQHNSFE
                                                                                                                                                                                                                                                                                                                                                                                                   SRSINRTYIRPINEVTYATSLLA------DGYYHVRV-----PESNVKE-----
                                                                                                                                                                                                                                                                                                                                                                                                                                          ADEDSNAQVTTENQLKYLTRLLGVEGTTLREALTHRKIIAKGEELLSPLNLEQAAYARDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RYTYKNTIDDKTIYISGINNE-----IIDLQKD-LWKYLSIV-GVIVLFTVYLA 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEKEITNIAHNEKNIILIKEKDKDKIIYS -- SGNIKDIDHRIDNEANPSKLINKNTKLGM 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----ETMCSSMNPIMAQCFDK--SELSDKKRPETVATQFKMSLLQLVEILRSKEPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative 106;
                                                             -SIKGFAETLIEGAKNDEQSLDMFLNIILKES--NRIESLVTDLLDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.3%; Score 126; DB 4; Length 567; 18.4%; Pred. No. 0.0048;
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520 318

362

462

361

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243

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Query Match Best Local Similarity 19.7%; Pred. No. 0.024; Matches 195; Conservative 143; Mismatches 392; Indels 260; Gaps 44;  Qy 138 YAETCPAPERGGAVRDRLLOSNPVLEAFGNAKTLRNDNSSRF 179 Db 38 WAETIPYGEPGISSPVSGGWDTSTWGLKSNTEPQSPPIASPKAITKPVRRTTVVDESENFF 97  Qy 180 GKYMDOOFDEKGAPVGGHILSYLLEKSRVVHQNHGERNFHVFVOLLEGGEEETLRRL 236 Db 98 SAFLSPTDVQTIQKSPVYSKPPAKS	Oy 630 LGLMENLEWRAGEP	Db 407 SHIEOOKELEINYMNI SELATUTTANI CTO
SULT 14 -09-356 sequence Patent No APPLICAN CONTROL TITLE OF FILE REF FILE NO CURRENT CUR		

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-356-952-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 2.3%; Score 123.5; DB 3; Length 1333; Best Local Similarity 18.3%; Pred. No. 0.037; Matches 212; Conservative 175; Mismatches 369; Indels 405;
                                                                                                                                                                                                                                                                                                                                                                                                                                          528
  771
                                                                                                                                                                   661 ---IAIENGDQPLSAELKRFRKEYIQPVQLRVLNVCR--HWVEHHFYDFERDAYLLQRME 715
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       248 RIVDIHELSVKLIGHIEDTVENTDEGSPHPLVGSCFEDLAEELAFDPYESYARDILRPGF 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               149 VRNIRHYEITKQDIKVAMCADK------VLMDMFHQDVEDI-----NILS 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       108 E---KIHPLLKEVLGYKIDHQVSVY------IVAVLEYISADILKLVG-----NY 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                130 ATKRLLQFYAETCPA-PERGGAVRDRLLQS--NPVLE-AFGNAKTLRNDNSSRFGKYMDV 185 :|: :| :|: :| :|: :| :|
                                                                                                                                                                                                                  702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            188 LTDEEPSTSGEQTYYDLVKAFMAEIRQYIRELNLIIKVFREPFVSNSKLFSANDVENIFS 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 AADED-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51 ---LILQLLMMLCQAQPRSASDVEERVQKSFPHPIDKWAIADAQSAIEKRKRRNPLSLPV 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     70 PYRDLQIYSRQHMERYRGVSFYEVPPHLFAVADTVYRALRTERRDQAVMISGESGAGKTE 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7 PY---EFFSEENAPKWRGL----LVPALKKVQGQVHPTL--ESNDDALQYVEE------
IETFDLLTLHPIEIARQLTLLESDLYRAVQPSELVGSVWTKEDKEINSPNLLKMIRHTTN 830
                                                                                                                                                                                                            KTLFATED-----SLEVRR-----QSLATKIQAAWRGFHW-RQKFLRVKRSAICIQSW- 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ESPSWRSTTVLGLLDIY-GFEVFQHNSF-----EQFCINYCNE-KLQQLFIELTLKSEQ 439
                                      VRASFLLNLR-----RQL------PRNVLDTSWP-----TPPPALR-----
                                                                          EFIGTV--RGKAMKKW-VESITKIIQRKKIARDNGPGHNITFQSSP--PTVEWHISRPGH
                                                                                                                           -WRGTLGRRKAAKRKWAAQTIRRLIR-------GFILRHSPRCPENAFFLD---H 792
                                                                                                                                                                                                                                                         YADPNEVRTELTTYRSFC-----KPQELLSLIIERFEIPEPEPTEADR------
                                                                                                                                                                                                                                                                                                 FAYRRKYEAFLQRYKSLCPETWPMWAGRPQDGVAVLVRHLGY-KPEEYKMGRTKIFIRFP 701
                                                                                                                                                                                                                                                                                                                                                LPSADVYRFAEP------DSEENIIFEENMQPKAGIPIIKAGTVIKLIERLTYHM--
                                                                                                                                                                                                                                                                                                                                                                                         LQLVEILRSKEPAYIRCIKPNDAKQPGRFDE-----VLIRHQVKYLGLMENLRVRRAG 642
                                                                                                                                                                                                                                                                                                                                                                                                                                     AKSAEEKNNWMAALISLQYRSTLERM------LDVTMLQEEKE-----EQMR 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VTGFLDKNN-----DLLFRNLKETMCSSMNPIMAQCFDKSELSDKKRPETVATQFKMSL 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAEYRLKEKFFMRKVQINDKDDTNEYKHAFEIILKDENS------VIFS 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T-----DLTFLEKLE----DTVKPHPHFLTHKLADQKTRKSLDRGEFRLLHYAGEVTYS 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IQKNIDGWEGKDIGQCCNEFIMEGTLTRVGAKHERHIFLFDGLMICCKSNHGQPRLPGAS 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EEYEAEGIAWEPVQYFNNKIICD----LVEEKFKGIISILD--EECLR------PGEA 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EDKECLKQAITALLNVQSGMEKICSKSLAKRRLSESACRFYSQQMKGKQLAIK---KMNE 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HDRFLSQLSKPGAALYLQSIGEGFKEAVQYVLPRLLLAPVYHCLHYFELLKQLEEKSEDQ 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----TRLLG-VEGTT--LREALTHRKIIAKGEELLSPLNLE-QAAYARDALAKAV 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            L----YLVKGQCAKVSSINDKSDWKVMRKALSVIDFTEDEVEDLLSIVASVLHLGNIHF 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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KTE 129	ESGAGK	DOAVMISGI	70 PYRDIOIYSROHMERYRGVSFYEVDDHLEAVADUVVBALRUFBRADOAVMISGESGAG	
Gaps	425;	Indels		Matches
	1319;	Length :	atch 2.3%; Score 122.5; DB 2;	Query
				us-08-2
			TOPOLOGY: linear LECULE TYPE: protein	<u>x</u>
			ino acid	•
			EQUENCE CHARACTERISTICS: LENGTH: 1319 amino acids	 
			~	; INFO
			TELEX: 6491103	
			ri ···	
,	\ <sup>1</sup>		COMMUNICATION INFORMATION:	TI
			REFERENCE/DOCKET NUMBER: 30,764	
		-	NAME: KIT, Gordon	
		•	TORNEY AGENT INFORMATION:	 <u>&gt;</u>
			LICATION NU	••
			PRIOR APPLICATION DATA:	id.
			PCT	
			-	; PI
			FILING DATE: 1/-OCT-1994 CLASSIFICATION: 435	
			CATION NO	
			SOFIMARE. FACEBLIA RELEASE #1.0, VEISION #1.25 CURRENT APPLICATION DATA:	Ω.
			SYSTEM: PC-DOS/MS-DOS	
			COMPUTER: IBM PC compatible	•••
			MEDIUM TYPE: Floory disk	c
			20037	1
			COUNTRY: USA	`
			J &	
			100 PENNSYLVANIA AVENUE, N.W.	
			ADDRESSEE: STIGHRITE MTON, SINN, MACCEAK & SEAS	
			ENCES: 15	
		•	OF INVENTION: AND mSOS POLYPEPTIDES	113
		· E	TITLE OF INVENTION: DNA MOLECULES ENCODING MURINE TITLE OF INVENTION: SON OF SEVENLESS (MSOS) GENE.	
		1	CANT: BOWTELL, David Douglas Lawrence	A
			INFORMATION:	GENERAL
			nce 2, Application US/08290731C L No. 5843646	Sequence; Patent No
			10.	RESULT
			.002 EKEFTDYLFNKSLEIEPRNPK 1022	Db 10
			51 -SSLSDSLFVLHVQREDNKQK 970	Оу 9
SM 100	LNPMGN	ESDIKRFFENLNPMGNSM	51 HGKELINESKRRKVAEITGEIQQYQNQPYCLRVESDI	Db 9
ISV 950	ANLTGI	IVEDAKVKQRIDYANLTG	IPSAVV	Оу 8
KR 950	GNPEVL	TNILKTEE	QKKILEEAHELSE	Db 8
QS 894	ISPRVL	RLFISTRLGTEEISPRVLQS	SO QQLQQKAVASEIFKGKKDNYPQSVPRLFIST	Оу 8
TF 890	VYRLDH	VSAMNSSP	31 LTLWFEKCIVETENLEERVAVVSRIIEILQVFQELNNFNGVLEVVSAMNSSPVYRLDHTF	Db 8
849	SPEWK	4	23EASELLRELCMXNMVWXXCRSt-   :: :       : ::	QΫ́
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RSI 844 :: 880 SAMNS 880 TRLGT 884	RR	941	
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9 8 8 8	EEISPRVLQSLGSEPIQYAVPVVKYDRKGYKPRPRQLLLTPSAVVIVEDAKVKQRI	о о	
<b>80 80</b>	SPEWKQQLQQKAVASEIFKGKKDNYPQSVPRLFISTRLGT	845 881	
	ALR	820 821	
-TPPP 819	PRNVLDTSWP   : :     ESDLYRAVQPSELVGSVWTKEDKET	786 761	
PRCPE 785	RSAICIOSWWRGTLGRRKAAKRKWAAQTIRRLIRGFILRHSPRC	740 706	
ELRVK 739   :   FYDFE 705	GRTKIFIRFPKTLFATEDSLEVRROSLATKIQAAWRGFHW-RQKFLRV	69 <b>2</b>	
EEYKM 691   : EPTEA 658	MENLRVRRAGFAYRRKYEAFLQRYKSLCPETWPMWAGRPQDGVAVLVRHLGY-KPEEYKM :	610	
KYLGL 632     TVLKL 609	TVATQFKMSLLQLVEILRSKEPAYIRCIKPNDAKQPGRFDEVLIRHQVKYLGL	580 565	
KKRPE 579 :  EKE 564	LHYAGEVTYSVTGFLDKNNDLLFRNLKETMCSSMNPIMAQCFDKSELSDKKRP	526 518	
L 525 : AFEII 517	PGEATDLTELEKLEDTYKPHPHFLTHKLADQKTRKSLDRGEFR	482 476	
LR 481 : CKSNH 475	IELTLKSEQEEYEAEGIAWEPVQYFNNKIICDLVEEKFKGIISILDEECLR-	431 419	
KLQQLF 430   :   KGKQLA 418	QHNSFEQFCINYCNE- 	379 361	
LVRKI 378  :::: LLKQL 360	DALAKAVYSRTFTWLVRK	360 301	
QAAYAR 359 :    YESYAR 300	QLKYLTRLLG-VEGTTLREALTHRKIIAKGEELLSPLNLE-QAAYAR::::	315 241	
VTTEN 314 : :   LFSSN 240	HLGNIHFAADEDSNAQVTTEN	294 184	
VASVL 293	ERNPQSYLYLVKGQCAKVSSINDKSDWKVMRKALSVIDFTEDEVEDLLSIVA : :	239 147	
RRLGL 238 : :  KLVG- 146	QFDFKGAPVGGHILSYLLEKSRVVHQNHGERNFHVEYQLLEGGEEETLRRLG :	101	
КҮМDV 185 100	ATKRLLQFYAETCPA-PERGGAVRDRLLQSNPVLE-AFGNAKTLRNDNSSRFGKYMDV	130 51	

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Db 992 ENLNPMGNGMEKEFTDYLFNKSLEIEPRHPK 1022

Search completed: December 9, 2002, 16:48:40 Job time : 37~secs

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Database :
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB seq length: 2000000000
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Published_Applications_AA:*

1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

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6: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

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10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*

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Gapop 10.0 , Gapext 0.5
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5398
1 MRYRASALGSDGVRVTMESA.....LITKAKNGHLAVVAPRLNSR 1044
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Copyright (c) 1993 - 2002 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

19	18	17	16	15	14	13	12	11	10	9	00	7	6	· G	4	ω	2	1	Result No.	
136.5	137.5	140	144.5	144.5	144.5	145.5	148	150.5	150.5	207.5	215.5	497	566	568	1105	1186	1240	1261.5	Score	
2.5	2.5	2.6	2.7	2.7	2.7	2.7	2.7	2.8	2.8	3. 8	4.0	9.2	10.5	10.5	20.5	22.0	23.0	23.4	Query Match	æ
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Sequence 42606, A	Sequence 42604, A	Sequence, 41891, A	Sequence 760, App	Sequence 41762, A	Sequence 39854, A	Sequence 1, Appli	Sequence 48341, A	Sequence 41932, A	Sequence 34208, A	Sequence 937, App	Sequence 923, App	Sequence 3, Appli	Sequence 551, App	Sequence 686, App	Sequence 1, Appli	Sequence 1583, Ap	Sequence 1, Appli	Sequence 2, Appli	Description	

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115.5	115.5	115.5	115.5	115.5	11.7	117	117	119	120.5	120.5	121	122	122	122	122	122	122	122.5	123.5	123.5	125	129.5	130	130.5	133.5
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US-09-736-969A-96	US-09-736-968A-110	US-09-736-960-13	US-09-736-969A-13	US-09-736-968A-13	US-10-017-216-2	US-09-815-242-13698	US-09-864-761-38637	US-09-864-761-37176	US-09-815-242-11238	US-10-055-364-40	US-09-864-761-42566	US-10-028-158-23	US-09-833-790-235	US-09-922-958-4	US-09-902-941-330	US-09-736-457-330	US-09-864-761-42178	US-09-727-384-6	US-10-028-946-2	US-10-028-946-4	US-09-864-761-47524	US-09-864-761-40482	US-09-815-242-13312	US-09-864-761-42111	US-09-815-242-10617
96,	10,	Sequence 13, Appl	Sequence 13, Appl	Sequence 13, Appl	Sequence 2, Appli	Sequence 13698, A	Sequence 38637, A	Sequence 37176, A	Sequence 11238, A	Sequence 40, Appl	Sequence 42566, A	Sequence 23, Appl	Sequence 235, App	Sequence 4, Appli	Sequence 330, App	Sequence 330, App	Sequence 42178, A	Sequence 6, Appli	Sequence 2, Appli	Sequence 4, Appli	Sequence 47524, A	Sequence 40482, A	Sequence 13312, A	Sequence 42111, A	Sequence 10617, A

## ALIGNMENTS

12;

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Sequence 1, Application US/10044303

Patent No. US20020137161A1

GENERAL INFORMATION:
APPLICANT: Max-Planck-Gesellschaft e.V.
TITLE OF INVENTION: Protein expression and structure sol.
TITLE OF INVENTION: Specific fusion vectors
FILE REFERENCE: ST010209-EPB.
CURRENT APPLICATION NUMBER: US/10/044,303

CURRENT FILING DATE: 2002-01-11

NUMBER OF SEQ ID NOS: 3

SOFTWARE: Patentin Ver. 2.1

LENGTH: 765
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE: TARGEDMANTION: Proceedings of the control of the con
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RSAICIQSWW----RGTLGRRKAAKRKWAAQTIRRLIRGFILRHSPRCPENAFFLDHVRA
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                                                                       Description of Artificial Sequence: Partial Sequence of Dictyostellum; Component (1) of recombinant protein M761-2R R238E
           23.0%;
  Score 1240;
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Length
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CURRENT APPLICATION NUMBER: US/09/925,300
CUBRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1583
LENGTH: 569
TYPE: PRT
                                                                                                                                                                                                                                                             RESULT 3
US-09-925-300-1583
; Sequence 1583, Application US/09925300
; Patent No. US20020151681A1
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                                                                                                                                                                                              FILE REFERENCE: PA101
                                                                                                                                                                                                        TITLE OF INVENTION: Nucleic Acids, Proteins
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 ORGANISM: Homo
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RYQQTKSSALVIQSYIRGWKARKILRELKHQKRCKE 538
                                                                          FIRFPKTLFATEDSLEVRRQSLATKIQAAWRGFHWRQKFLRVKRSAICIQSWWRGTLGRR 756
                                                                                                          RVRRAGYAFRQAYEPCLERYKMLCKQTWPHWKGPARSGVEVLFNELEIPVEEYSFGRSKI
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                            KAAKRKWAAQTIRRLIRGF-----ILRHSPRCPE 785
                                                      FIRNPRTLEKLEDLRKQRLEDLATLIQKIYRGWKCRTHFLLMKKSQIVIAAWYRRYAQQK
                                                                                                                                         RVRRAGFAYRRKYEAFLQRYKSLCPETWPMWAGRPQDGVAVLVRHLGYKPEEYKMGRTKI 696
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                                                                                                                                                                       RPPTAGSQFKASVATLMKNLQTXXPNYIRCIKPNDKKAAHIFNEALVCHQIRYLGLLENV
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47.1%; Pred. No. 1.6e-85;
tive 86; Mismatches 167;
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RESULT 4 US-09-851-682A-1

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; ORGANISM: Homo sapier US-09-851-682A-1
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APPLICANT: Welch, Juliet
TITLE OF INVENTION: MYOSIN IXA AND CYCLIC NUCLEOTIDE GATED
TITLE OF INVENTION: CHANNEL-15 (CNGC-15) POLYNUCLEOTIDES, PC
TITLE OF INVENTION: COMPOSITIONS, METHODS, AND USES THEREOF
FILE REFERENCE: 200130 442
CURRENT APPLICATION NUMBER: US/09/851,682A
CURRENT FILING DATE: 2001-05-08
PRIOR APPLICATION NUMBER: US/09/172,422
PRIOR APPLICATION STEP 10-14
NUMBER OF SEO ID NOS: 3
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SMDSFSFLQHPVHQRSLEILQRCKEEKYSITRKNPRTPLSDLQGMNALNEKNQHDTFDIA
                                                                             LRSSKNAFISGMIGIDPVAVFRWAILRAFFRAMVAFREAGKRNIHRKTGHDDTAPCAILK 739
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Duhl, David
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Leng, Song
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US-09-925-302-686
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US-09-925-302-686
; Sequence 686, Application US/09925302
; Patent No. US20020044941A1
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              Query Match
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SEQ ID NO 686
LENGTH: 245
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and
FILE REFERENCE: PA104
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                                                        OTHER INFORMATION:
                                                                         NAME/KEY: SITE
LOCATION: (145)
                                                                                                               ORGANISM: Homo sapiens
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   Score 568;
                                    naturally occurring L-amino acids
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US-09-764-853-551
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Patent NO. US20020090672A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and
FILE REFREENCE: PJ206
CURRENT APPLICATION NUMBER: US/09/764,853
CURRENT FILING DATE: 2001-01-17
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SEQ ID NO 551
LENGTH: 570
TYPE: PRT
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Best Local 9
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SOFTWARE: PatentIn Ver. 2.0
Best Local Similarity 52.1 Matches 112; Conservative
                                           359 AAAITGDSAEAMPAPMHCGRTKVFM-----TDSMLELLECGRARVLE------
                                                                      674 GVAVLVRHLGYKPEEYKMGRTKIFIRFPKTLFATEDSLEVRROSLATKIQAAWRGFHWRQ
                                                                                                    299 SHRNFVERYKLLRRLHPCTSSGPDSPYPAKGLPEWCPHSEEATLEPLIQDILHTLPVLTQ
                                                                                                                                     648 KYEAFLQRYKSL-----C----PET-----WPMWAGRPQD-----
                                                                                                                                                                                  588 SLLQLVEILRSKEPAYIRCIKPNDAKQPGRFDEVLIRHQVKYLGLMENLRVRRAGFAYRR
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                                                                                                                                                                                                                                                                                                 479 CL--RPGEATDLTFLEKLEDTYKPHPHFLTHKLADQKTRKSLDRGEFRLLHYAGEVTYSV 536
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                                                                                                                                                                                                                                                                                                                                                                                                               359 RDALAKAVYSRTETWLVRKINRSLASKDABSPSWRSTTVLGLLDIYGFEVFQHNSFEQFC 418
                                                                                                                                                                                                                                                                                                                                     69 INYANEKLOOHEVAHYLRAQQEEYAVEGLEWSFINYQDNQPCLDLIEGSDISICSLINEE
                                                                                                                                                                                                                                                                                                                                                                                              14 RDCLAKLIYARLEDWLVSVINSSIC---ADTDSW--TTFIGLLDVYGFESEPDNSLEQLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             508 KLADQKTRKSLDRGEFRLLHYAGEVTYSVTGFLDKNNDLLFRNLKETMCSSMNPIMAQCF 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   448 AWEPVQYFNNKIICDLVEEKFKGIISILDEECLRPGEATDLTFLEKLEDTVKPHPHFLTH 507
                                                                                                                                                            SLEQLLQVLHSTTPHYIRCIKPNSQGQAQTFLQEEVLSQLEACGLVETIHISAAGFPIRV
                                                                                                                                                                                                                                                 TGFLDKNNDLLFRNLKETMCSSMNPINAQCF--DKSELSDKKRPE-----TVATQFKM 587
                                                                                                                                                                                                                                                                              CRLNRPSSAAQLQ--TRIETALAGSPCLGHNKLSREPS-----FIVVHYAGPVRYHT 178
                                                                                                                                                                                                                                                                                                                                                                INYCNEKLOOLFIELTLKSEQEEYEAEGIAWEPVQYFNNKIICDLVEEKFKGIISILDEE 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       167;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10.5%; Score 566; DB 10; 27.6%; Pred. No. 1.2e-36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               91;
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3; Mismatches 66;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 570;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 150;
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                 792
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                                                                                                                                                                                                                                                                                                                                                                                               83
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Query Match 9.2%; Score 497; DB 10; Length 2568; Best Local Similarity 22.6%; Pred. No. 3.3e-30; Matches 266; Conservative 194; Mismatches 439; Indels 280; Gaps 51;	: LENGTH: 2568 ; TYPE: PRT ; ORGANISM: Homo sapiens US-09-866-108-3	: 2001-02-05 NOS: 15752 Sequence Li	FILING DATE: 2001-01-30 APPLICATION NUMBER: US FILING DATE: 2000-09-21 APPLICATION NUMBER: US	FILING DATE: 2001-01-30 APPLICATION NUMBER: PCT/US01 FILING DATE: 2001-01-30 APPLICATION NUMBER: PCT/US01	FILING DATE: 2001-01-30 APPLICATION NUMBER: PCT/US01 FILING DATE: 2001-01-30 APPLICATION NUMBER: PCT/US01		FILING DATE: APPLICATION N FILING DATE: APPLICATION N	FILING DATE: 2000-09-27 APPLICATION NUMBER: PCT FILING DATE: 2001-01-30 APPLICATION NUMBER: PCT	FILING DATE: 2000-05-20 APPLICATION NUMBER: GB FILING DATE: 2000-10-0 APPLICATION NUMBER: US	REFERENCE: AEOMICA-7 NIT APPLICATION NUMBER: US/09/866,108 NIT FILING DATE: 2001-05-25 APPLICATION NUMBER: US 60/207,456	RANK, David R. CHEN, Wensheng SHANNON, Mark NVENTION: MYOSIN		US-09-866-108-3 : Sequence 3, Application US/09866108 : Patent No. US20020048800A1 : GENERAL INFORMATION:	Db 516 GSFQRK 521 RESULT 7	Db 461 RMACLAAKELDGVEEKHFSQAPCSLSTSPLQTRLLEAIIRFWPLGLVLANTAMGV 515  QY 907 VKYDRK 912	853 QQKAVASEIFKGKKDNYPQSVPRLFISTRLGTEEISPRVLQSLGSEPIQYAVPV	441 IQKUHAAATVIKRAWQKWRI	Db 401KH 440  Qy 793 VRASFLLNLRRQLPRNVLDTSWPTPPPALREASELLRELCMKNMVWKYCRSISPEWKQQL 852
QY 000 INLG TELESER TO WASHED THE REPORT FOR THE PROPERTY OF T	828 LRELCMKNMVWKYCRSISPEWKQQLQQKAVASEIFKGKKDNYPQSVPRLFIS  1479 KSKHEQVQKKLGDVMKQ-LEZAQQKIQLNDLERDDTGGADEWQMRFDCAQMENEFLR	Qy 773 RGFILRHSPRCPENAFFLDHVRASFLLNLRQLPRNVLDTSWPTPPPALREASEL 827 :   :   :   :   :   :	Qy 737 RVKR-SAICIQSWWRGTLGRRKAAKRKWAAQTIRR-LI 772   :::	Qy 683 GYKPEEYKMGRTKIFIRFPKTLFATEDSLEVRRQSLATKIQAAWRGFHWRQKFL 736 : :   ::: ::     : :     :	Qy 634 ENLRVRRAGFAYRRKYEAFLQRYKSLCPETWPMWAGRPQDGVAVLVRHL 682	Qy 596 LRSKEPAYIRCIKPNDAKQPGRFDEVLIRHQVKYLGLM 633 :	Qy 558SMNPIMAQCFDKSELSDKKRPETVATOFKMSLLQLVEI 595	Qy 511 DQKTRKSLDRGEFRLLHYAGEVTYSVTGFLDKNNDLLFRNLKETMCS 557 : :	Qy 466EKFKGIISILDEECLRPGEATDLTFLEKLEDTVKPHPHFLTHKLA 510	Qy 417 FCINYCNEKLQQLFIELTLKSEQEEYEAEGIAWEPVQYFNNKIICDLVE 465	Qy 363 AKAVYSRTFTWLVRKINRSLASKDAESPSWRSTTVLGLLDIYGFEVFQHNSFEQ 416	Oy 317 KYLTRLLGVEGTTLREA-LTHRKIIAKGEELLSPLNLEQAAYARDAL 362	Qy 261 DKSDWKVMRKALSVIDFTEDEVEDLLSIVASVLHLGNIHFAADEDSNAQVTTENQL 316	OY 209 VHONHGERNFHVFYQLLEGGEEETLRRLGLERNPQSYLYLVKGQCAKVSSI 260	QY 149 GAVRDRLLQSNPVLEAFGNAKTLRNDNSSRFGKYMDVQFDFKGAPVGGHILSYLLEKSRV 208	631 GLPAHIGSMAQRAYWALLNQRRDQSIVALGRSGAGKTTCCEQVLEHLVGMAGSVD-G	89	Qy 29 VQDFVLLENFTSEAAFIENLRRRFRENLIYTYIGPVLVSVNPYRDLQIYSRQHWERYRGV 88

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RESULT 9
US-09-925-299-937
Sequence 937, Application US/09925299
Patent No. US20020055627A1
GENERAL INFORMATION:
APPLICANT: ROSEN et al.
TITLE OF INVENTION: Nucleic Acids, Proteins
FILE REFERENCE: PAI02
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; ORGANISM: Homo sapiens
US-09-925-301-923
CURRENT APPLICATION NUMBER: US/09/925,299 CURRENT FILING DATE: 2001-08-10 PRIOR APPLICATION NUMBER: PCT/US00/05883 PRIOR FILING DATE: 2000-03-08 PRIOR APPLICATION NUMBER: 60/124,270 PRIOR FILING DATE: 1999-03-12
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US-09-925-301-923
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Nucleic Acids, Proteins FILE REFERENCE: PA106 CURRENT APPLICATION NUMBER: US/09/925,301 CURRENT FILING DATE: 2001-08-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/124,270 PRIOR FILING DATE: 1999-03-12 NUMBER OF SEQ ID NOS: 1694
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: PCT/US00/05882 PHIOR FILING DATE: 2000-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 923,
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APPLICANT: Rosen et al.
                                                                                                                                                                                                                                                                                                                     1038 A 1038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                            933 DAKVKQRIDYANLTGISVSSLSDSLEVLHVQR-EDNKQKGDVVLQSDHVIETLTK---TA 988
                                                                                                                                                                                                                                                                                       294 A 294
                                                                                                                                                                                                                                                                                                                                          242 LSQTKQKLNIEISDEFLVQFRQDKVCVKFIQGNQKNGSVP-
                                                                                                                                                                                                                                                                                                                                                                  989 LSADRVN-NINI-----NQGSITFAGGPGRDGIIDFTSGSELLITKAKNGHLAVV 1037
                                                                                                                                                                                                                                                                                                                                                                                                     182 SGOIKSEVPLVDVTKVSMSSONDGFFAVHLKEGSEAASKGDFLFSSDHLIENATKLYRTT 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 GAYL---EINKNPKYKKLKDAIEEKIIIAEVVNKINRANGKSTSRIFLLTNNNLLLADQK 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          879 STRLGTEEISD----RVLQSLGSEPIQYAVPVVKYDRKGYKPRPRQLLLTPSAVVIVE-- 932
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             822 REASELLRELCMKNMVW----KYCRSISPEWKQQLQQKAVASEIFKGKKDNYPQSVPRLFI 878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 763 WAAQTIRRLIRGFILRHSPRCPENAFFLDHVRASFLLNLRRQLPR-NVLDTSWETPPPAL 821
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1646 QQQLKQKEQEASQLKQQVEMLQDHKRELLGSPSLGENCV 1684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LDSTH--KELKRIFHLWRCKKYRDQFTDQQKLIYEEKLEASELFKDKKALYPSSVGQPFQ 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WLGLKVRREYRKFFRANAGK-KTYEFTLQRIVQKYFLEMKNKMPSLSPIDKNWPSRPYLF 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | : |::
| EDTCVLLENQOSRNHELEKKOKKFDLQLAQALGESVFEKGLREKVTQENTSVRWELGQL 1645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.0%; Score 215.5; DB:
26.6%; Pred. No. 1.8e-09;
ative 55; Mismatches 127
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                                                                                                            and Antibodies
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PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
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LOCATION: (79)
OTHER INFORMATION: xaa equals any of the naturally occurring L-amino .
NAME/KEY: SITE
LOCATION: (85)
OTHER INFORMATION: xaa equals any of the naturally occurring L-amino US-09-925-299-937
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APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT APPLILING DATE: 2001-05-23
CURRENT TATELLING DATE: 2001-05-23
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Best Local
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 937
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 147 ALQTIFNRWRASQLIKSIPASDLPQVRAKVAAVEMLKGQRADLGLQRAWEGNYLASKP 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     827 LLRELCMKNMVWKYCRSISPEWKOOLOOKAVASEIFKGKK------DNYPOSVP 874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             767 TIRRLIRGFILRHSDRCPENAFFLDHVRASFLLNLRRQLPRNVLDTSWPTPDPPALREASE 826
APPLICATION NUMBER: PCT/US01/00668 FILING DATE: 2001-01-30
                                           APPLICATION NUMBER: PCT/US01/00665
FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        649 YEAFLORYKSLCPETWPMWAGRPQDGVAV--LVRHLGYKPEEYKMGRTKIFIRFPKTLEA 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          707 TEDSLEVRROSLATKIQAAWRGFHWRQKFLRVKRSAICIQSWWRGTLGRRKAAKRKWAAQ 766
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Hanzel, David K.
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.71
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 4.6
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.64
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.96
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.71
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.1
OTHER INFORMATION: EXTRESSED IN HEART, SIGNAL = 1.10
OTHER INFORMATION: EXTRESSED IN HEART, SIGNAL = 1.00-56
OTHER INFORMATION: EXTRESSED IN HEART, SIGNAL = 3.00-56
OTHER INFORMATION: EXTRESSED IN HEART, SIGNAL = 1.10-20
OTHER INFORMATION: EXTRESSED IN HEART, SIGN
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Best Local :
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                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: Aeomica-X-1
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TYPE: PRT
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APPLICATION NUMBER: PCT/US01/00670
TITING DATE: 2001-01-30
                               APPLICATION NUMBER: US 60/236,359
FILING DATE: 2000-09-27
APPLICATION NUMBER: PCT/US01/00666
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FILING DATE:
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Pred. No. 4.6e-05;
4; Mismatches 43
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; OTHER INFORMATION: MAP TO AL049829.3; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.7; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 69; OTHER INFORMATION: SWISSPROT HIT: P13533, EVALUE 3.00e-56; OTHER INFORMATION: EST_HUMAN HIT: F00635.1, EVALUE 3.00e-28 US-09-864-761-41932
                                                          CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR APPLICATION NUMBER: US 99/632,366
PRIOR APPLICATION NUMBER: US 99/632,366
PRIOR APPLICATION NUMBER: US 99/632,366
PRIOR APPLICATION NUMBER: US 98/632,366
PRIOR APPLICATION NUMBER: US 98/633,66
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Best Local Similarity
Matches 41; Conserv
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                                                                                                                                                                                                                                                                 APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
FILE REFERENCE: Acomica-X-1
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                                           PRIOR
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PRIOR APPLICATION NUMBER: PCT/US01/00670
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                   60/236,359
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Pred. No. 4.6e-05;
4; Mismatches 43
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APPLICATION NUMBER: FILING DATE: 2001-01

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RESULT 13
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                                                                           SOFTWARE: PatentIn Ver.
SEQ ID NO 1
LENGTH: 1337
TYPE: PRT
                                                                                                                                                                                   APPLICANT: Brooks, Alan R.
APPLICANT: Deng, Gary G.
APPLICANT: Rubanyl, Gabbor M.
TITLE OF INVENTION: Estrogen-Regulated Unconventional Myosin-Related
TITLE OF INVENTION: Protein: Compositions and Methods of Use
FILE REFERENCE: 015303-000310US
CURRENT APPLICATION NUMBER: US/09/803,126
CURRENT FILING DATE: 2001-03-09
CURRENT FILING DATE: 1001-03-09
                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US Patent No. US20020099190A1
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Best Local
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ORGANISM: Homo saplens
ORGANISM: Homo saplens
FEATURE:
OTHER INFORMATION: EXPRI
OTHER INFORMATION: EXPRI
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                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/188,488 PRIOR FILING DATE: 2000-03-10
FEATURE:
OTHER INFORMATION: mouse myosin related protein (MRP)
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                                                           ORGANISM: Mus sp
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FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00665
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EXPRESSED IN BONE MARROW, SIGNAL = 5.7

EXPRESSED IN LUNG, SIGNAL = 3.8

SWISSPROT HIT: P34092, EVALUE 4.00e-14

EST_HUMAN HIT: BE513695.1, EVALUE 5.00e-16
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RESULT 14
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                             APPLICATION NUMBER: US
FILING DATE: 2000-09-21
APPLICATION NUMBER: US
FILING DATE: 2000-06-30
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APPLICATION NUMBER: US FILING DATE: 2001-01-29
                                                                                      APPLICATION NUMBER: PCT/US01/00670 FILING DATE: 2001-01-30
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FILING DATE: 2001-01-30
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APPLICATION NUMBER: GB
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                                                                                                                                                                                               APPLICATION NUMBER: PCT/US01/00663
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Hanzel, Wensheng
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David K.
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                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US:09/632,366
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILE REFERENCE: Aeomica-X-1
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SEQ ID NO 39854
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CURRENT FILING DATE: 2001-05-23
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                                                  FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00665
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Pred. No. 0.00013;
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LENGTH: 102
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Best Local
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PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
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ORGANISM: Homo sapiens
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                               522 EFRLLHYAGEVTYSVTGFLDKNNDLLFRNLKETMCSSMNPIMAQCFDKSELSD 574
50 HFALIHYAGVVDYNITGWLEKNKDPLNETVVGLYQKSAMKTLAQLFSGAQTAE 102
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APPLICATION NUMBER: PCT/US01/00661
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SWISSPROT
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IN HEART, SIGNAL = 2.4
IN ADULT LIVER, SIGNAL = 2.4
HIT: F00185.1, EVALUE 5.00e-26
HIT: P13535, EVALUE 4.00e-50
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IN HELA, SIGNAL = 1.9
IN BONE MARROW, SIGNAL = 4.6
IN LUNG, SIGNAL = 1.7
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Pred. No. 0.00013;
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Search completed: December 9, 2002, 16:55:10 Job time : 26 secs

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RESULT 2
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myosin I beta - human
C:Species: Homo saplens (man)
C:Species: Homo saplens (man)
C:Species: Homo saplens (man)
C:Species: Homo saplens (man)
C:Cobate: 19-May-2000 #sequence_revision 19-May-2000 #text_change 08-Sep-2000
C:Accession: A59253
R:Crozet, F.; Amraoul, A.E.; Blanchard, S.; Lenoir, M.; Ripoll, C.; Vago, P.; Hamel, C.;
A;Roference number: A59253; MUID:97237053; PMID:9119401
A;Rofession: A59253
A;Status: preliminary; not compared with conceptual translation
A;Rofession: RNAA
A;Residues: 1-1028 <CRO>
A;Cross-references: GB:X98507; NID:g1926310; PIDN:CAA67131.1; PID:g1926311
A;Proceimantal source: day stage adult: tissue type kidney
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A;Gene: myo-lb
A;Map position: 17p3.2-p13.3
C;Superfamily: brush border myosin heavy chain I; my F;14-683/Domain: myosin motor domain homology <MMO>
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                                  95.3%; Score 5143; I
llarity 96.2%; Pred. No. 0;
Conservative 23; Mismatches
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                                  16;
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A; Molecule type: mRNA
A; Residues: 1-6, 'C',8-96,'R',98-221,'PGT',223-281,'N',283-296,'GTSSST',303,'PGPWVWR',307
721,'L',723-909,'WSF',913,916-988,'SSQ',992-994,'AGMASLTSH',1004,'ARSCSSPRPRT',1016,'TWA; Cross-references: EMBL:Z22852
A; Cross-references: EMBL:Z22852
C; Keywords: actin binding; ATP; calmodulin binding; nucleotide binding; P-loop
F;14-683/Domain: myosin motor domain homology <MMOT>
F;105-112/Region: nucleotide-binding motor domain homology
F;376-595/Region: actin binding #status predicted
F;699-743/Region: actin binding #status predicted
F;699-743/Region: calmodulin binding #status predicted
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N;Alternate names: myosin IB heavy chain
C;Species: Bos primianning to the chain
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A;Description: Domain structure of a mammalian myosin I (bovine myosin A;Reference number: $33497
A;Accession: $33497
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A; Residues: 1-1028 <ZHU>
A; Cross-references: GB:U03420; NID:g436936; PIDN:AAA17565.1;
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A;Residues: 1-6,'C',8-96,'R',98-319,'N',321-362,'K',364-385,'D',387-543,'I',545-549,'F'
A;Cross-references: GB:222852; NID:g397402; PIDN:CAA80476.1; PID:g397403
A;Experimental source: brain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Species: Bos primigenius taurus (cattle);Date: 20-May-1994 #sequence_revision 02-Jun-1995 #text_change 02-Feb-2001;Accession: S41749; A55744; S33497
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                 KINRSLASKDAESPSWRSTTVLGLLDIYGFEVFQHNSFEQFCINYCNEKLQQLFIELTLK 436
                                                                                                         KYLTRLLGVEGTTLREALTHRKIIAKGEELLSPLNLEQAAYARDALAKAVYSRTETWLVR 376
                                                                                                                                                                                                                                                          HILSYLLEKSRVVHQNHGERNFHIFYQLLEGGEEETLRRLGLERNPQSYLYLVKGQCAKV
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); MUID:94148088; PMID:8313976
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A;Gene: AMI beta
A;Introns: 639/2
A;Introns: 639/2
C;Superfamily: brush border myosin heavy chain I;
C;Keywords: nucleotide binding; P-loop
E;14-683/Domain: myosin motor domain homology <MMC
E;105-112/Region: nucleotide-binding motif A (P-Lo
                                                                                                                                                                                                                      R:Metcalf, A.B.; Chelliah, Y.; Hudspeth, A.J. Proc. Natl. Acad. Sci. U.S.A. 91, 11821-11825, 1994 A;Title: Molecular cloning of a myosin I beta isozyme A;Reference number: IS1173, MUID:95083594; PMID:799154 A;Accession: I51173
                                                                                                                                             A;Cross-references:
C;Genetics:
                                                                                                                                                                                                                                                                                                     myosin I beta - bullfrog
C;Species: Rana catesbeiana (bullfrog)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change
C;Accession: I51173
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A; Residues: 1-1028 <M
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81.0%;
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Score 4371;
Pred. No. 7.
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Query Match

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RESULT 5
H75634
myosin-Ic - mouse (fragment)
N;Alternate names: myosin-I beta
C:Species: Mus musculus (house mouse)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 08-9
C;Accession: H75634
R:Corzet, F: Amraoui, A.E.; Blanchard, S.; Lenoir, M.; Ripoll, C.;
Genomics 40, 332-341, 1997
A;Title: Cloning of the genes encoding two murine and human cochlean
A;Reference number: A59253; MUID:97237053; PMID:9119401
A;Status: preliminary; not compared with conceptual translation
A:Molecule tune. mpwn
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A;Cross-references: MGI:106612
A;Map position: 11:44.1
C;Superfamily: brush border myosin heavy
F;14-683/Domain: myosin motor domain home
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A; Residues: 1-807 <CRO>
A; Cross-references: GB: X99638; NID:g1924960;
A; Experimental source: strain BALB/c; tissue
C; Genetics:
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                                                                               RFDEVLIRHQVKYLGLMENLRVRRAGFAYRRKYEAFLQRYKSLCPETWPMWAGRPQDGVA
                                         RFDEVLIRHQVKYLGLMENLRVRRAGFAYRRKYEAFLQRYKSLCPETWPMWAGRPQDGVA
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type cochlea; dev stage adult
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R:Strom Morgan, N.; Skovronsky, D.M.; Artavanis-Tsakonas, S.; Mooseker, M.S.
J. Mol. Blol. 239, 347-356, 1994
A;Title: The molecular cloning and characterization of Drosophila melanogaster:
A;Reference number: $45573; MUID:94260541; PMID:8201616
A;Accession: $45574
A;Accession: $45574
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1026 <STR>
A;Cross-references: GB:U07596; NID:9466257; PIDN:AAA19591.1; PID:9466258
C;Superfamily: brush border myosin heavy chain I; myosin motor domain homology
C;Keywords: nucleotide binding; P-loop
F;14-681/Domain: myosin motor domain homology <NMOT>
F;105-112/Region: nucleotide-binding motif A (P-loop)
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$45574

sydson IB - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Accession: S45574
R; Strom-Morgan, N.;
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                                                                                                                                                                                                                               RLNISLQAKETRA---SRNNVMGILDIYGFEIFQKNSFEQFCINFCNEKLQQLFIELTLK
                                                                                                                                                                                                                                                  KINRSLASKDAESPSWRSTTVLGLLDIYGFEVFQHNSFEQFCINYCNEKLQQLFIELTLK 436
                                                                                                                                                                                                                                                                                                                                               KYLTRLLGVEGTTLREALTHRKIIAKGEELLSPLNLEQAAYARDALAKAVYSRTETWLVR 376
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SSMNPIMAQCFDKSELSDKKRPETVATQFKMSLLQLVEILRSKEPAYIRCIKPNDAKQPG
                                               KLAQHHHYVCHEKAPAHIKKIMLRDEFRLVHYAGEVTYSVNGFLDKNNDLLFRDLKETLS
                                                                    VTAARLLGVNASELEAALTHRTIDARGDVVTSPLNQELAIYARDALAKAVYDRLFSWLVQ
                                                                                                                                                                                                                                                                                                                                                                                                               TSINDADSFKQVQQALTVIDFGKEEQREIFGIVASILHLGNVGF-TEVEGNAKVNSRDLV
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51.5%; Pred. No. 2.1e-160;
tive 177; Mismatches 300;
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C;Species: Mus musculus (house mouse)
C;Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change
C;Accession: B45438
R;Sherr, E.H.; Joyce, M.P.; Greene, L.A.
J. Cell Biol. 120, 1405-1416, 1993
A.;Title: Mammalian myosin I alpha, I beta, and I gamma: new wide
A;Reference number: A45438; MUID:93194946; pMID:8449986
A;Accession: B45438
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Residues: 1-448 CSHE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Note: sequence extracted from NCBI backbone (NCBIP:131911) C;Superfamily: brush border myosin heavy chain I; myosin motor domain F;1-448/Domain: myosin motor domain homology (fragment) <MMOT>
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                                                                                                                                                                                                         YQLLEGGEEETLRRLGLERNPQSYLYLVKGQCAKVSSINDKSDWKVMRKALSVIDFTEDE 281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KGEELLSPLNLEQAAYARDALAKAYYSRTFTWLVRKINRSLASKDAESPSWRSTTVLGLL 401
                                                                                       VEDLLSIVASVLHLGNIHFAADEDSNAQVTTENQLKYLTRLLGVEGTTLREALTHRKIIA 180
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KGEELLSPLNLEQAAYARDALAKAVYSATFTWLVRKINRSVPAKDAESPSWRSTTVLGLL
                                                                                                                                                                                  YQLLEGGEEEALRRLGLERNPQSYLYLVKGQFAKVSSINDKSDWKLLRKALSVIDFTEDE 120
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                                                                                                                                                                                                                                                                                                                                                                    435;
                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                     41.78;
97.18;
                                                                                                                                                                                                                                                                                                                                                               Score 2252; DB 2;
Pred. No. 1.3e-136;
6; Mismatches 7;
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                                                                                                                                                                                                                                                                                                                                                                                                          Length 448;
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Matches Query Match

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497

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360

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homology

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Qy 443 EAEGIAWEPVQYFNNKIICDLVEEKFKGIISILDEECLRPGEATDLTFLEKLEDTVK	383 ASKDAESPSWRSTTVLGLLDIYGFEVFQHNSFEQFCINYCNEKLQOLFIELTLKSE :	323 LOVEGTTLREALTHRKIIAKGEELLSPLNLEQAAYARDALAKAVYSRTETWLVRK	267 VMRKALSVIDETEDEVEDLLSIVASVLHLGNIHFAADEDSNAQVTTENQLKY :    : :   :     :   :	207 RVVHQNHGERNFHVEYQLLEGGEEETLRRLGLERNPQSYLYLVKGQCAKVSSINT	147 RGGAVEDRLLQSNPVLEAFGNAKTLRNDNSSREGKYMDVQEDEKGAPVGGHILS 	87 GVSFYEVPHLEAVADTVYRALRTERRDQAVMISGESGAGKTEATKRLLQFYAETC 	27 VGVQDEVLLENETSEAAFIENLRRRFRENLIYTYIGPVLVSVNPYRDLQIYSRC 15 IGVGDTVLLEPL-NEETFIDNLKKRFDHNEIYTYIGSVVISVNPYRSLPIYSPE	Ouery Match 39.1%: Score 2109; DB 2; Length 1078; Best Local Similarity 42.8%; Pred. No. 7.5e-127; Matches 463; Conservative 183; Mismatches 346; Indels 90	Lecule type: mRNA; protein sidues: 1-1078 <rup> sidues: 1-1078 <rup> Le: sequence extracted from NCBI backbone (NCBIN:128956, NCBIF perfamily: brush border myosin heavy chain I; myosin motor dom'ywords: nucleotide binding; p-loop -688/Domain: myosin motor domain homology <mmot> 8-115/Region: nucleotide-binding motif A (P-loop)</mmot></rup></rup>	<pre>Cert Blot. 120, 1393-1403, 1993 Pitle: Identification, characterizat Reference number: A45439; MUID:93194 Accession: B45439 Status: preliminary</pre>	5439 Osin-I, Myr Ic (alternatively spliced) - rat Species: Rattus norvegicus (Norway rat) Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 0 Accession: B45439 Accession: B45439 Accession: B45439 Accession: B45439	SULT 8	82 ATQFKMSLLQLVEILRSKEPAYIRCIKP	361 EFRILHYAGEVTYSVTGFLDKNNDLLFRNLKETMCSSTNPIMAQCFDKSELSDKK	GEVTYSVTGFLDKNNDLLFRNLKETMCSSMNPIMAQCFDKSELSDKK	TOWERFRENT   TOWN   T	241 DIYGFEVFQHNSFEQFCINYCNEKLRQLFIELTLKSEQEEYE	
LEKLEDTV      LEKLNQVC	FIELTLKE	RTFTWLVRKINRSL 382    :   :    : RLFSWLVNRINESI 372	NELK NOLK	CAKVSSINDKSDWK 266     : ::  :::: SAKVNGVDDAANFR 252	PVGGHILSYLLEKS 206  :     :       PLGGVISNYLLEKS 193	RLLOFYAETCPAPE 146 :: :		gth 1078 dels 9	956, NC	myr 1,	_change			FDKSELSDKKRPETV 4	ELSDKKRPETV 58		H ~	

	1075 VA 1076	ob 10
	1037 VA 1038	2y 10
1074	1023 TLSQTKQKLNIEISDEFLVQFRQDKYCVKFIQGNQKNGSVPTCKRKNNRLLE 1	Db 10
1036	988 ALSADRVN-NININQGSITFAGGGPGRDGIIDFTSGSELLITKAKNGHLAV 1036	Ωу 9
1022	963 KSGQIKSEVPLVDVTKVSMSSQNDGFFAVHLKEGSEAASKGDFLFSSDHLIEMATKLYRT :	Db 9
987	933 -DAKVKQRIDYANLTGISVSSLSDSLFVLHVQR-EDNKQKGDVVLQSDHVIETLTKT	Qy 9
962	906 QGAYLEINKNPKYKKLKDAIEEKIIIAEVVNKINRANGKSTSRIFLLTNNNLLLADQ	Db 9
932	878 ISTRIGTEEISPRVLQSLGSEPIQYAVPVVKYDRKGYKPRPRQLLLTPSAVVIVE-	Ωу е
905	848 FLDSTHKELKRIFHLWRCKKYRDQFTDQQKLIYEEKLEASELFKDKKALYPSSVGQPF	Db 6
877	821 LREASELLRELCMKNMVWKYCRSISPEWKQQLQQKAVASEIFKGKKDNYPQSVPRLF 877	Оу 8
847	788 AYWHGTQVRREYRKFFRANAGKKIYEFTLQRIVQKYLLEMKNKMDSLSDIDKNWPSRPYL	Db 7
820	788	Qy
787	728 KRSQVVIAAWYRRYAQQKRYQQIKSSALVIQSYIRGWKARKILRELKHQKRCKEAATTIA	Db
787		Qy .
727	668 FNELEIPVEEYSFGRSKIFIRNPRTLFQLEDLRKQRLEDLATLIQKIYRGWKCRTHFLLM	Db
738	679 VRHLGYKPEEYKMGRTKIFIREPKTLFATEDSLEVRRQSLATKIQAAWRGFHWRQKFLRV	Qy
667	608 SESIVCHQIRYLGLLENVRVRRAGYAFRQAYEPCLERYKMLCKQTWPHWKGPARSGVEVL	Db
678	619 DEVLIRHQVKYLGLMENLRVRRAGFAYRRKYEAFLQRYKSLCPETWPMWAGRPQDGVAVL	Qy
607	548 ALIKSLEPEGNPAKVNLKRPPTAGSQFKASVATLMKNLQTKNPNYIRCIKPNDKKAAHIF 607	рb
618	561 PIMAQCEDKSELSDKKRPETVATQFKMSLLQLVEILRSKEPAYIRCIKPNDAKQPGRF 618	Qу
547	488 HFESRMSKCSRFLNDTTLPHSCFRIQHYAGKVLYQVEGFVDKNNDLLYRDLSQAMMKAGH 547	DЬ
560	503 HFLTHKLADQKTRKSLDRGEFRLLHYAGEVTYSVTGFLDKNNDLLFRNLKETMCSSMN	γ

Qy Dр

Дb Qγ

В Qy DЬ QΥ Ъ γQ рь δÃ

RESULT 9
A29483
myoSin heavy chain I, brush border - bovine
N;Alternate names: myoSin I heavy chain-like protein, MIHC
N;Contains: myoSin ATPase (EC 3.6.4.1)
C;Species: Bos primigenius taurus (cattle)
C;Date: 31-Dec-1993 #sequence\_revision 31-Dec-1993 #text\_change 19-Apr-2002
C;Accession: A29483; JX0208
R;HOShimaru, M; Nakanishi, S.
J. Biol. Chem. 262, 14625-14632, 1987
A;Title: Identification of a new type of mammalian myosin heavy chain by molecular cl
A;Reference number: A29483; MUID:88033016; PMID:3667594
A;Accession: A29483
A.McCession: A29483

A: Nolecule type: mRNA
A: Residues: 1-1043 <HOS>
A: Cross-references: GB:J02819; NID:g163405; PIDN:AAA30658.1; PID:g163406
A: Cross-references: GB:J0281, A: Cross-references: GB:J0281, NID:g163405; PIDN:AAA30658.1; PID:g163406
A: Reference number: JX0208; MUID:g2268028; PMID:1587791
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             --PIQYAVPVVKYDRKGYKPRPRQLLLTPSAVVI--VEDAKVKQRIDYANLTGISVSSLS
                                                                                                                          FLDHVRASFLLNLRRQLPR-NVLDTSWPTPP----PALREASELLRELCMKNMVWKYCR 842
                                                                                                                                                                                            VKRSAICIOSWWRGTLGRRKAAKRKWAAQTIRRLIRGFILRHSPR-----
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                                            KFRDQLSPKQVEVLREKLCASELFKGKKASYPQSVPIPFHGDYIGLQR-NPKLQKLKGGE
                                                                       ----SISPEWKQQLQQKAVASEIFKGKKDNYPQSVPRLFISTRLGTEEISPRVLQSLGSE
                                                                                                     YKSMVQ-KFLLGLKNDLPSPSILDKKWPSAPYKYFNTANHELQRLFHQ-----
                                                                                                                                                               MRKSQIVISSWFRGNMQKKHYRKMKASALLIQAFVRGWKARKNYRKYFRSGAALILSNFI 779
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A;Molecule type: mRNA; p
A;Residues: 1-1107 <RUP>
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C; Species: Rattus norvegicus (Norway rat)
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GVSFYEVPPHLFAVADTVYRALRTERRDQAVMISGESGAGKTEATKRLLQFYAETCPAPE
:|||: ||:||::| ||:||::| ||
RRFYELSPHIFALSDEAYRSLRDQDKDQCILITGESGAGKTEASKLVMSYVAAVCGKGA
                                                                                                                             EAEGIAWEPVQYFNNKIICDLVEEKFKGIISILDEECLRPGEATDLTFLEKLEDTVKPHP
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                                                                             HFLTH--KLADQKTRKSLDRGEFRLLHYAGEVTYSVTGFLDKNNDLLFRNLKETMCSSMN
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A; Molecule type: nucleic acid
A; Residues: 1-1079 <SHE>
A; Cross-references: GB:L00923; NID:g200008; PIDN:AAA39800.1; PID:g200009
A; Experimental source: brain
A; Note: sequence extracted from NCBI backbone (NCBIN:129047, NCBIP:129048)
C; Superfamily: brush border myosin heavy chain I; myosin motor domain homology
C; Koywords: nucleotide binding; P-loop
F;18-689/Domain: myosin motor domain homology <NMOT>
F;108-115/Region: nucleotide-binding motif A (P-loop)
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A45438

MA5438

myosin I alpha chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 02-Feb-2001
C:Accession: A45438
C:Accession: A45438
                                                                                                                                                                                                                                                                                                                                                                             R;Sherr, E.H.; Joyce, M.P.; Greene, L.A.
J. Cell Biol. 120, 1405-1416, 1993
A;Title: Mammalian myosin I alpha, I beta, and I gamma: new widely expressed genes A;Reference number: A45438; MUID:93194946; PMID:8449986
A;Accession: A45438
A;Status: preliminary
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                                                                        QR-EDNKOKGDVVLQSDHVIETLTK---TALSADRVN-NINI------NQGSTTFA 1007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PVVKYDRKGYKPRPRQLLLTPSAVVIVE--DAKVKQRIDVANLTGISVSSLSDSLFVLHV 962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KLIYEEKLEASELFKDKKALYPSSVGQPFQGAYL --- EINKNPKYKKLKDAIEEKIIIAE
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                                                                                                                                                  Indels 93;
                                                                                                                                                                                  Length 1079;
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	  LEVA 1077	1074	Dβ
		1035	Qy
1073		1022	Db.
1034		987	Qy
1021	QKSGQIKSEVPLVDVTKVSMSSQNDGFFAVHLKEGSEAASKGDFLFSSDHLIEMATKLY	962	Db
5		932	VΩ
61		905	Db
931		876	Qy
904	YLFLDSTHKELKRIFHLWRCKKYRDQFTDQQKLIYEEKLEASELFKDKKALYPSSVGQ 9	847	Δp
875	LRELCMKNMVWKYCRSISPEWKQQLQQKAVASEIFKGKKDNYPQSVPR	819	Qy
846	IAAYWLGLKVRREYRKFFRANAGKKIYEFTLQRIVQKYLLEMKNKMPSLSPIDKNWPSRP 8	787	Db
818	РP	788	Qy
7 <sup>8</sup> 6	LMKRSQVVIAAWYRRYAQQKRYQQIKSSALVIQSYIRGWKARKILRELKHQKRCKEAATT	727	DЬ
787		737	Qу
726		667	Db
736	Ľ	677	Qy
666		607	Db
676	REDEVLIRHQVKYLGLMENLRVRRAGFAYRRKYEAFLQRYKSLCPETWPMWAGRPQDGVA	617	Qy
606	DHSTIKSLEPEGNPAKVNLKREPTAGSQFKASVATLMRNLQTKNPNYIRCIKPNDKKAAH	547	DЬ
616	MNPIMAQCFDKSELSDKKRPETVATQFKMSLLQLVEILRSKEPAYIRCIKPNDAKQPG	559	Qγ
546	HOHFESRMSKCSRFLNDTTLPHSCFRIQHYAGKVLYQVEGFVDKNNDLLYRDLSQAMWKA	487	Db
558	HPHFLTHKLADQKTRKSLDRGEFRLLHYAGEVTYSVTGFLDKNNDLLFRNLKETMCSS	501	Qy
486	EYIREDIEWTHIDYFNNAIICDLIENNTNGILAMLDEECLRPGTVTDETFLEKLNQVCAT	427	DЪ
500	EYEAEGIAWEPVQYFNNKIICDLVEEKFKGIISILDEECLRPGEATDLTFLEKLEDTVKP	441	Qу
426	SIKAQTKVRKKVMGVLDIYGFEIFEDNSFEQFIINYCNEKLQQIFIELTLKEEQE	372	В
440	SLASKDAESPSWRSTTVLGLLDIYGFEVFQHNSFEQFCINYCNEKLQQLFIELTLKSEQE	381	Qy
371		313	Db
380		321	Qy
312	TVRNAMQIVGFLDHEAEAVLEVVAAVLKLGNIEFKPESRVNGL	253	Db
N		267	Qy
252	4 RVVKQPRGERNFHVFYQ1LSGASEELLYKLKLERDFSRYNYL-SLDSAKVNGVDDAANFR	194	DЪ
266		207	Qy
193	4 EVNQVKEQLLQSNPVLEAFGNAKTVRNDNSSRFGKYMDIEFDFKGDPLGGVISNYLLEKS	134	Db
206		14/	Š

myosin I heavy chain - rat
C:Species: Rattus norvegicus (Norway rat)

RESULT A45439

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submitted to the EMBL Data Library, September 1992
A:Reference number: S29984
A:Reference number: S29984
A:Accession: S29984
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1136 <RU2>
A:MOLecule type: mRNA
A:Residues: 1-1136 <RU2>
A:Cross-references: EMBL:X68199; NID:956732; PIDN:CAA48287.1; PID:956733
A:Cross-references: EMBL:X68199; NID:956732; PIDN:CAA48287.1; PID:956733
C:Superfamily: brush border myosin heavy chain I; myosin motor domain hon C:Keywords: nucleotide binding; P-loop
F:18-688/Domain: myosin motor domain honology <MMOT>
F:18-688/Domain: myosin motor domain honology <MMOT>
F:108-115/Region: nucleotide-binding motif A (P-loop)
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R:Ruppert, C.; Kroschewski, R.; Bahler, M.
J. Cell Biol. 120, 1393-1403, 1993
A:Title: Identification, characterization and cloning of A:Reference number: A45439; MUID:93194945; PMID:8449985
A:Accession: A45439
A:Status: preliminary
A:Molecule type: mRNA; protein
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A;Residues: 1-1136 <RUP>
A;Residues: 1-1136 <RUP>
A;Cross-references: GB:X68199; NID:g56732; PIDN:CAA48287.1; PID:g56733
A;Note: sequence extracted from NCBI backbone (NCBIN:128956, NCBIP:128961)
R;Ruppert, C.
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EAEGIAWEPVQYFNNKIICDLVEEKFKGIISILDEECLRPGEATDLTFLEKLEDTVKPHP 502
                                                                                                                                                                                                                                                                                                                                                                           ASKDAESPSWRSTTVLGLLDIYGFEVFQHNSFEQFCINYCNEKLQQLFIELTLKSEQEEY 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VGVQDFVLLENFTSEAAFIENLRRRFRENLIYTYIGPVLVSVNPYRDLQIYSRQHMERYR 86
                                                                                      ALIKSLEPEGNPAKVNLKRPPTAGSQFKASVATLMKNLQTKNPNYIRCIKPNDKKAAHIF
                                                                                                                                                                                                   HFLTH--KLADQKTRKSLDRGEFRLLHYAGEVTYSVTGFLDKNNDLLFRNLKETMCSSMN 560
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RVVHQNHGERNFHVFYQLLEGGEEETLRRLGLERNPQSYLYLVKGQCAKVSSINDKSDWK 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NRNFYELSPHIFALSDEAYRSLRDQDKDQCILITGESGAGKTEASKLVMSYVAAVCGKGA 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IGVGDTVLLEPL-NEETFIDNLKKRFDHNEIYTYIGSVVISVNPYRSLPIYSPEKVEDYR 73
                                                                                                                               PIMAQCFDKSELS--DKKRPETVATQFKMSLLQLVEILRSKEPAYIRCIKPNDAKQPGRF 618
                                                                                                                                                                          HFESRMSKCSRFLNDTTLPHSCFRIQHYAGKVLYQVEGFVDKNNDLLYRDLSQAMWKAGH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LGVEGTTLREALTHRKIIAKGEELLSPLNLEQAAYARDALAKAVYSRTFTWLVRKINRSL 382
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RVVKQPRGERNFHVFYQLLSGASEELLHKLKLERDFSRYNYL-SLDSAKVNGVDDAANFR 252
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40.6%; Pred. No. 5
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5.9e-125;
hes 346;
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Que Bees Matt Qy Db Qy Qy Db	C; Spe C; Data C; Acc C; Acc C; Acc FBS FEBS A; Rel A; Rel A; Res Submin A; Res A; Res A; Res A; Res C; C; C	Db (Qy ) (Qy	Qy
Query Match  38.4%; Score 2075.5; DB 2; Length 1094; Best Local Similarity 41.9%; pred. No. 11e-124; Matches 464; Conservative 184; Mismatches 348; Indels 112; G  2 VGVQDFVLLENETSEAAFIENLRRRERENLIYTYIGPVLVSVNPYRDLQIYSRQHMERYR  2 IGVQDMVLLEPL-NEETFIDNLKKRFDHNERYTYIGSVVISVNPYRSLPIYSPEKVEDYR  387 GVSFYEVPPHLFAVADTVVRALRTERRDQAVMISGESGAGKTEATKRLQFYAETCPAPE  388 GVSFYEVPPHLFAVADTVVRALRTERRDQAVMISGESGAGKTEATKRLQFYAETCPAPE  389 GVSFYEVPPHLFAVADTVVRALRTERRDQAVMISGESGAGKTEATKRLQFYAETCPAPE  390 GVSFYEVPPHLFAVADTVRALRTERRDDAVGGGTTESTGESGAGKTEASKLVMSYVAAVCGKGA  391 H:   :  :  :  :  :  :  :  :  :  :  :  :	C. Species: Mus musculus (house mouse) C. Date: 03-May 1994 #sequence_revision 20-Feb-1995 #text_change 02- C. Accession: S32404; S33973 R: Koslovsky, J.S.; Oian, C.; Jiang, X.; Mercer, J.A. FEBS Lett. 320, 121-124, 1993 A; Title: Molecular cloning of a mouse myosin I expressed in brain. A; Reference number: S32404; MUJD:93209370; PMID:8458427 A; Accession: S32404 A; Molecule type: mRNA A; Residues: 1-1094 <kos> A; Cross-references: EMBL:X69987; NID:g312270; PIDN:CAA49604.1; PID: R; Mercer, J.A. submitted to the EMBL Data Library, January 1993 A; Recession: S33973 A; Recession: S33973 A; Recession: S33973 A; Recession: S33973 A; Recroule type: mRNA A; Residues: 1-572, 'G', 574-762, 'G', 764-1094 <mer> A; Cross-references: EMBL:X69987 C; Superfamily: brush border myosin heavy chain I; myosin motor doma C; Keywords: nucleotide binding; P-loop F; 5-675/Domain: myosin motor domain homology <mmot> F; 95-102/Region: nucleotide-binding motif A (P-loop)</mmot></mer></kos>	668 FNELEIPVEEYSFGRSKIFIRNPRTLFQLEDLRKQRLEDLATLIQKIYRGWKCRTHFLLM 739 KRSAICIQSWWRGTLGRRKAAKRKWAAQTIRRLIRGFILRHSPRCPENA	679 VRHLGYKPEEYKMGRTKIFIRFPKTLFATEDSLEVRRQSLATKIQAAWRGFHWRQ
4; ; Gaps 2: ERYR 86         EDYR 60 PAPE 146 GKGA 120 LEKS 206	in. pID:g1666471		FLRV 738

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myosin heavy chain I, brush border - chicken N:Contains: myosin ATPase (EC 3.6.4.1) C:Species: Gallus gallus (chicken) C:Date: 31-Dec-1993 #sequence_revision 31-Dec
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                                                                                                                                                                     KEGSEAASKGDFLFSSDHLIEMATKLYRTTLSQTKQKLNIEI---SDEFLVQFRQDKVCV
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C;Accession: A33620
R;Garcia, A.; Coudrier, E.; Carboni, J.; Anderson, J.; Vandekerkhove, J.; Mooseker, J. Cell Biol. 109, 2895-2903, 1989
A;Title: Partial deduced sequence of the 110-kD-calmodulin complex of the avian int A;Reference number: A33620; MUID:90078325; PMID:2687288
A;Accession: A33620
A;Molecule type: mRNA
A;Residues: 1-1000 <GAR>
A;Cross-references: GB:S6479; NID:963075; PIDN:CAA41388.1; PID:963076
C;Superfamily: brush border myosin heavy chain I; myosin motor domain homology
C;Keywords: actin binding; hydrolase; intestine; nucleotide binding; P-loop
F;59-66/Region: nucleotide-binding motif A (P-loop)
F;530-551/Region: actin binding #status predicted
F;65/Binding site: ATP (Lys) #status predicted
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41.6%;
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Pred. No. 9.2e-114;
1; Mismatches 358;
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R:Baehler, M.; Kroschewski, R.; Stoeffler, H.E.; Behrmann, T. Cell Biol. 126, 375-389, 1994 A;Title: Ratt myr 4 defines a novel subclass of myosin I: identification A; Reference number: A53933; MUID:94308268; PMID:8034741 A;Reference number: A53933; MUID:94308268; PMID:8034741 A;Reference number: A53933; MUID:9516395; PID:9516396 A;Croses'references: GB:X71997; NID:9516395; PID:9516395; PID:9516396; PID:9516395; PID:951639
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	L 945	945	Db
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94	MKTIPLYNLTGLSVSNGKDQLVVFHT - KDNKDLIVCLFSKQPTHESRIGE	896	Дb
99	KORIDYANLIGISVSSLSDSLFVLHVOREDNKOKGDVVLQSDHVIETLIKTALSADRVNN 99	937	Qy
89	LKRKDKYMNVLFSCHVRKVNRFSKVEDRAIFVTDRHLYKMDPTKQYKV	848	DЬ
93	KYBRKGYKPRPRQLLLTPSAVVIVEDAKV	908	Qy
84	PQVRAKVAAMEMLKGQRADLGLQRAWEGNYLASKPDTPQTSGTFVPVANE	798	망
90		850	Qy
79	SYTHEVARREHGVKNMRDYGKHVKWPTPPKVLRRFEEALQSTFNRWRASQLIKTTPASDL 79	738	Db
84		796	Qy
73		700	, Db
79	LRVKRSAICIOSWWRGTLGRRKAAKRKWAAQTIRRLIRGFILRHSPRCPENAFFLDHVRA 79	736	Qy
69	KKLIERCGFQ-DDVAYGKTKIFIRTPRTLFTLEELRAQMLV	660	DЬ
73		678	Qy
65	FDDERGRHQVEYLGLLENVRVRRAGFAFRQTYEKFLHRYKMISEFTWPN-HDLPSDKEAV	601	Db
67		618	Qy
60	PVLKNMWPERKLSITEVTKRPLTAATLFKNSMIALVDNLASKEPYYVRCIKPNDKKSPQI	541	DЬ
61	PIMAQCEDKSELSDKKRPETVATQEKMSLLQLVEILRSKEPAYIRCIKPNDAKQPGR 61	561	Qy
54		482	DЬ
56	HPHFLTHKLADQKTRKSLDRGEFRLLHYAGEVTYSVTGFLDKNNDLLFRNLKETMCSSMN 56	501	Qy

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"Cloning of the genes encoding two murine and human cochlear

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Y "Mammallan myosin I alpha, I beta, and I gamma: new widely expressed greenes of the myosin I family.";

Quenes of the myosin I family.";

C-1- FUNCTION: MYOSINS ARE ACTIN-BASED MOTOR MOLECULES WITH ATPASE ACTIVITY. UNCONVENTIONAL MYOSINS SERVE IN INTRACELLULAR MOVEMENTS.

C THEIR HIGHLY DIVERGENT TAILS ARE PRESUMED TO BIND TO MEMBRANOUS COMPARTMENTS, WHICH WOULD BE MOVED RELATIVE TO ACTIN FILAMENTS (BY SIMILARITY).

C-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A (SHOWN HERE) AND B; ARE PRODUCED BY ALTERNATIVE SPLICING.

C-1- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.

C-1- SIMILARITY: CONTAINS 2 10 DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U96723; AAC53264.1; ...
EMBL; MK004743; BAB23524.1; ...
EMBL; M96726; AAC60758.1; ...
EMBL; M96726; AAC60758.1; ...
HSSP CORPOSE CAA67956.1; ...
InterPro: IPR001609; Myosin_head; InterPro: IPR001609; Myosin_head; 1.
Pfam; PF000612; IQ; 3.
PRINTS; PR00193; MYOSINHEAVY.
PRODOM: PD000355; MYOSINHEAVY.
PRODOM: PD000355; MYOSIN-head; 1.
SMART; SM00015; IQ; 2.
SMART; SM00016; IQ; 2.
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CON
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Genomics 40:332-341(1997).
[4]
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ATP-binding; Actin-binding; Calmodulin-binding; ne family; Alternative splicing.
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PubMed=8449986;
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VMAPALANSA

IMPT (IN ISOFORM B)

RR -> GG (IN REF. 3).

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C -> F (IN REF. 4).

VM -> LL (IN REF. 4).

VM -> LL (IN REF. 4).

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VKP -> IKH (IN REF. 4).

VKP -> IKH (IN REF. 4).

VKP -> IKH (IN REF. 4).

VKP -> G (IN REF. 4).

S -> G (IN REF. 3).

R -> G (IN REF. 3).
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IQ 2.

ATP (POTENTIAL).

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                        SDHVIETLTKTALSADRVNNININOGSITFAGGFGRDGIIDFTSGSELLITKAKNGHLAV
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RESULT 2

MY1C_HUMAN

ID MY1C_HUMAN

AC 000159;
DT 16-0CT-2001

DT 16-0CT-2001

DT 16-0CT-2001

DE MYOSIN IC (!
GN MY01C.

OS HOMO Sapiens

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RC TISSUE-Kidn,

RX MEDLINE-972;

RA Hamel C., F

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InterPro; IPR001609; myosin_head.

Pfam; PF00605; myosin_head; 1.

Pfam; PF00605; Myosin_head; 1.

PRINTS; PF00612; IQ; 3.

PRODOM; PD000355; myosin_head; 1.

PRODOM; PD000355; myosin_head; 1.

PRODOM; PM000355; myosin_head; 1.

R MART; SM00015; IQ; 2.

R SMART; SM00015; IQ; 2.

R PROSITE; PS50096; IQ; 2.

W Myosin; ATP-binding; Actin-binding; Rep Multigene family.

M Multigene family.

1 683 MYOSIN HEAD-LIKE.
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Best Local s
Matches 989
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16-OCT-2001 (Rel. 40, I
16-OCT-2001 (Rel. 40, I
16-OCT-2001 (Rel. 40, I
Myosin IC (Myosin I bet
MYO1C.
Homo sapiens (Human).
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TISSUE-Kidney;
MEDLINE-97237053; PubMed-9119401;
Amraoui A.E., Blanchard S.,
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IO 2:
ATP (POTENTIAL).
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                     SDHVIETLTKTALSADRVNNININQGSITFAGGPGRDGIIDFTSGSELLITKAKNGHLAV
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RESULT 3

WY1B\_DROME STANDARD; PRT; 10

MY DROME STANDARD; PRT; 10

AC Q23979; 09W0H0;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence up

DT 15-UUN-2002 (Rel. 41, Last annotation

DE Myosin IB (MIB) (Brush border myosin I

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RA Bellew R.M., Basu A., An H.-J., Andrews Pfannkoch C., Baldwin D., RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Beasley E.M., RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Bortshakov S., RA Bortis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., Rodgon K., Debus D.A., Butler H., Cadieu E., Center A., Chandra I., RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W., RA Beer C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., RA Harris M.L., Harvey D., Helman T.J., Hernandez J.R., Houck J., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Alasko P., Lei Y., Levitsky A.A., L.J., Li Z., Liang Y., Lin X., Mattei B., McIntosh T.C., McLeod M.P., McBherson D., Lai Z., Markin D., Pittman G.S., Pan S., McLeod M.P., McBherson D.L., RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., RA RA Rainert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., RA Syler E., Siden-Klamos I., Simpson M., Strong R., Smith T., Ra RA Syler E., Stepadling A.C., Stapleton M., Strong R., Smith T., RA RA Syler E., Fertor C., Turner R., Venter E., Wang A. H., Wang X., RA Walliams S.M., Woodage T., Weinstock G.M., Weissenbach J., RA Ra Mang S.M., Wassarman D.A., Weinstock G.M., Weissenbach J., Ra Ra Mang S.M., Woodage T., Wools G., Zhao Q., Zheng L., The Glibbs R.A., Wyers E.W., Rubin G.M., Venter J.C., Sheng L., Smith H.O., The genome sequence of Drosophila melanogaster.", 51

R. Science 287:2185-2195(2000)
Morgan N.S., Heintzelman M.B., Mooseker M.S.; "Characterization of myosin-IA and myosin-IB, two urmyosins associated with the Drosophila brush border
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIJIND 9402500, MEDIJING, Verbsky J.w., Cheney C.M., Kravit N.G., Verbsky J.w., "A new myosin I gene in Drosophila."; "A new myosin I gene in Dr
                                                                                                                                                                                                                                                                                                                                                            FUNCTION,
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J. Mol. Biol. 239:347-356(1994).
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Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AND
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                                                                                                                                                                                                                                                                                                                    SPECIFICITY,
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                                                                        two unconventional
                                                                                                                                                                                                                                                                                                                           AND
             cytoskeleton.";
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61

137 FYAETCPAPERGGAVRDRLLQSNPVLEAFGNAKTLRNDNSSRFGKYMDVQFDFKGAPVGG

196 120

YTDDHVKAYRNKHFYEMPPHIFAVTDNAFRSLIEENRGQCVLISGESGSGKTEASKKVLQ

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                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00612; IQ; 3.
PRINTS; PR000193; MYOSINHEAVY.
ProDom; PD000355; MYOSIn_head;
                                                                                                                                                                                                                                                                                                                                                                                                                             FlyBase; FBg00010246; Myo61F.
InterPro; IPR000048; IQ_region.
InterPro; IPR001609; myosin_head.
Pfam; PF000663; myosin_head; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                              SMART; SM00015; IQ; 1.
SMART; SM00242; MYSC; 1.
                                                                                                                                                                                                                                                                                                                                    Myosin; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD
-!- SIMILARITY: CONTAINS 2 IQ DOMAINS.
-!- CAUTION: Ref.2 sequence differs from that shown of
                   77
                                                                                                 Local Similarity
mes 532; Conserv
                                    METGLHERDRAGVQDFVLLENYQSEEAFIGNLKKRFQEDLIYTYIGQVLISVNPYKQLPI
                                                      MESALTARDRYGYODFYLLENFTSEAAFIENLRRRFRENLIYTYIGPYLYSVNPYRDLQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEVELOPMENTAL STAGE: EXPRESSION STARTS AT 8-12 HOURS EMBRYONI DEVELOPMENT, CONTINUES TO INCREASE UNTIL THIRD LARVAL INSTAR, DISAPPEARS IN UPDAE AND IS PRESENT AT A LOW LEVEL IN ADULTS. EXPRESSION IN EMBRYOGENESIS IS CORRELATED WITH THE FORMATION BRUSH BORDER WITHIN THE ALIMENTARY CANAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7. Biol. 172:51-71(1995).

FUNCTION: INVOLVED IN DIRECTING THE MOVEMENT OF ORGANELLES ALONG ACTIN FILAMENTS (BY SIMILARITY).

SUBCELLULAR LOCATION: CYTOPLASMIC. PROTEIN SHIFTS FROM THE BASOLATERAL TO APICAL DOMAIN IN ENTEROCYTES AND FOLLICLE CELLS.

TISSUE SPECIFICITY: IN THE EMBRYO, EXPRESSED IN GASTRIC CAECAE, MIDGUT CELLS OF THE PROVENTRICULUS, AND IN THE MID AND HINDGUT.
YSROHMERYRGVSFYEVPPHLFAVADTVYRALRTERRDQAVMISGESGAGKTEATKRLLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene model prediction.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THE LARVAL AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  007596; AAA19591.1; AET_SEQ. AE003471; AAF47477.1; ALT_SEQ. L13070; , NOT_ANOTATED_CDS. AJ000879; CAA04367.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P08799;
                                                                                                                                                                                                                                                                                                                                                 PS50096; IQ;
                                                                                                                                                      697
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221
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                                                                                                             48.6%;
51.5%;
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                                                                                                                                                                                                                                                                                                   Calmodulin-binding; Actin-binding; Repeat.
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E PROVENTRICULUS, AND IN
LT GUT BRUSH BORDER, EXPR
XPRESSED AT HIGH LEVELS I
                                                                                               177;
                                                                                                                                             ACTIN BINDING (BY SIMILARITY)
D -> N (IN REF. 1).
R -> G (IN REF. 1).
R -> S (IN REF. 1).
T -> G (IN REF. 1).
S -> N (IN REF. 2).
EL -> DV (IN REF. 3).
D -> AI (IN REF. 3).
D -> AI (IN REF. 3).
                                                                                                                                                      ₩.
                                                                                                            Score 2626;
Pred. No. 4
                                                                                                                                                                                                                                                                          ATP (BY SIMILARITY)
                                                                                               Mismatches
                                                                                                          DB 1;
1.3e-159;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          that shown due to erroneous
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                                                                                                                      Length 1026;
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             (Brush border 110-kDa
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                                                                                                                                                      PGVVRDK-GHLVII 1023
                                                                                                                                                                LLITKAKNGHLAVV
                                                                                                                                                                                                                                                                                                                       KAVASEIFKGKKDNYPQSVPRLFISTRLGTEEI----SPRVLQSLGSEPIQYAVPVVKYDR
                                                                                                                                                                                                                                                                                                                                                                        ASFLLNLRRQLPRNVLDTSWPTPPPALREASELLRELCMKNMVWKYCRSISPEWKQQLQQ 854
                                                                                                                                                                                                                                                                                                                                                                                                                          FLRVKRSAICIQSWWRGTLGRRKAAKRKWAAQTIRRLIRGFILRHSPRCPENAFFLDHVR 794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQDEYRREGIEWIPVEYFONKVICNLIEEKHKGIISILDEECLRPGEPTDKTFLEKLTQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RLNISLQAKETRA---SRNNVMGILDIYGFEIFQKNSFEQFCINFCNEKLQQLFIELTLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KYLTRLLGVEGTTLREALTHRKIIAKGEELLSPLNLEQAAYARDALAKAVYSRTFTWLVR
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                                                                                                                                                                                                      DLKKDKGDLILIIPRIIEFSTYIIDTVGTASIVSIVDRNSLEHNVVKGKGGVIDIQTGAE
                                                                                                                                                                                                                                                       HGYKSRDRFILLSNKAIYVLDGKTYKQKHRLPLDKIDF-----TLTNHNDDLMVIRIPL
                                                                                                                                                                                                                                                                             KGYKPRPRQLLLTPSAVVIVEDAKVKQ-----RIDYANLTGISVSSLSDSLFVLHVQR 964
                                                                                                                                                                                                                                                                                                         KVLAEKVFKGKKNNYASSVSTWFQEDRIPKEHIQRVNDFVASTFGSEQLKYQSFCTKFDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FIAACSGNQTTVEGVKDKLLKSNPVLEAFGNAKTNRNDNSSRFGKYMDIQFDFKGAPIGG
                                                                                      STANDARD;
                      Last annotation update)
(BBM-I) (BBMI) (Myosin I
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           protein)
                                                 Last sequence update)
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ProDom; PD000355; myosin_head;
SMART; SM00015; TQ; 3.
SMART; SM00242; MYSC; 1.
PROSITE; PS50096; TQ; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no way.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000048; IQ_region.
InterPro; IPR001609; myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Biochem. 111:302-309(1992).
-!- FUNCTION: INVOLVED IN DIRECTING ACTIN FILAMENTS (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA."
                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                       PROSITE; PS50096; IQ; : Myosin; Actin-binding; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00063; myosin_head;
Pfam; PF00612; IQ; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A29483; A29483.
HSSP; P08799; 1MND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kawakami H., Moriyoshi K., Utsumi T., Nakanishi "Structural organization and expression of the G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-789
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Identification of a new type of mammalian myosin heavy chain molecular cloning. Overlap of its mRNA with preprotachykinin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE=88033016; PubMed=3667594;
                                                                                                                                                                                                                                                                               DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9913;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               taurus (Bovine).
QVNSVKEQLLQSNPVLEAFGNAKTIRNNNSSRFGKYMDIEFDFKGFPLGGVITNYLLEKS
          RGGAVRDRLLQSNPVLEAFGNAKTLRNDNSSRFGKYMDVQFDFKGAPVGGHILSYLLEKS : :|:::|||||||||||::|||||||||
                                               VGVQDEVLLENETSEAAFIENLRRRFRENLIYTYIGPVLVSVNPYRDLQIYSRQHMERYR
                                                                                                VGVEDLVLLEPLEQE-SLIRNLQLRYEKKEIYTYIGNVLVSVNPYQQLPIYDLEFVAKYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J02819; AAA30658.1;
                                                                                                                                                                Similarity
                                                                                                                                                                                                                  697
720
743
101
571
708
                                                                                                                                                   Conservative 185;
                                                                                                                                                                                                     ĀΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=1587791;
                                                                                                                                                                                                                             681
719
742
772
772
108
593
                                                                                                                                                               39.0%;
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                                                                                                                                                                                                                                                                                                                   ATP-binding; Calmodulin-binding;
                                                                                                                                                                                                              IQ 1.
IQ 2.
IQ 3.
ATP (BY SIMILARITY).
ACTIN-BINDING (POTENTIAL).
MISSING (IN REF. 2).
                                                                                                                                                                                                     MW;
                                                                                                                                                             Score 2106.5;
Pred. No. 4.5
                                                                                                                                                                                                                                                                                          MYOSIN
                                                                                                                                                    Mismatches
                                                                                                                                                                                                     581BE91EA508DB3C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THE MOVEMENT
                                                                                                                                                                                                                                                                                           HEAD-LIKE
                                                                                                                                                                4.5e-126;
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                                                                                                                                                                           DB 1;
                                                                                                                                                   330;
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gene
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                                                                                                                                                                           Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a collaboration - MBL outstation
                                                                                                                                                   65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               myosin
                                                                                                                                                 Gaps
                                                 126
                                                                        146
                                                                                                                           86
186
                      206
                                                                                                  66
                                                                                                                                                   21;
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RESULT 5
MY1A_MOUSE
ID AC P46735
DT 16-OCT
DT 15-JUN
DE MYOSIN
GN MYOSIN
OC EUKARY
OC MARMMAL
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                                                   MY1A_MOUSE STAN
P46735; P70244;
01-NOV-1995 (Rel. 3
16-OCT-2001 (Rel. 4
15-JUN-2002 (Rel. 4
Myosin IA (Myosin I
    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                             Mus musculus (Mouse)
                                                                                                                                                                         1010
                                                                                                                                                                                                                      950
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                                                                                                                                                                     GSLTVKVIQGPGGGG
                                                                                                                                                                                           GSIT--FAGGPGRDG
                                                                                                                                                                                                                                  DSLFVLHVQREDN-KQKGDVVLQSDHVIETLTK---TALSADRVN-----NININQ
                                                                                                                                                                                                            DGLFSLHLSEISSVGSKGEFLLVSEHVIELLTKICRATLDATQMQLPVTVTEEFSVKFKE
                                                                                                                                                                                                                                                                      --PIQYAVPVVKYDRKGYKPRPROLLLTPSAVVI--VEDAKVKQRIDYANLTGISVSSLS
                                                                                                                                                                                                                                                                                                      KFRDQLSPKQVEVLREKLCASELFKGKKASYPQSVPIPFHGDYIGLQR-NPKLQKLKGGE
                                                                                                                                                                                                                                                        ----SISPEWKQQLQQKAVASEIFKGKKDNYPQSVPRLFISTRLGTEEISPRVLQSLGSE
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                                                                                                                                                                                                                                                                                                                                                                                                              VKRSAICIQSWWRGTLGRRKAAKRKWAAQTIRRLIRGEILRHSDR------
                                                                                                                                                                                                                                                                                                                                                                                              MRKSQIVISSWERGNMQKKHYRKMKASALLIQAFVRGWKARKNYRKYFRSGAALILSNFI
                                                                                                                                                                                                                                                                                                                                                                                                                                          FDEVLIRHQVKYLGLMENLRVRRAGFAYRRKYEAFLQRYKSLCPETWPMWAGRPQDGVAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NPIMAQCEDKSE--LSDKKRPETVATQEKMSLLQLVEILRSKEPAYIRCIKPNDAKQPGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FSFELVSVQAQYLGLLENVRVRRAGYAYRQAYGSFLERYRLLSRSTWPRWNGGDQEGVEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HPLLRSLFPEGDPKQASLKRPPTAGAQFKSSVTTLMKNLYSKNPNYIRCIKPNEHQQRGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KREGIPWVKVEYFDNGIICNLIEHNQRGILAMLDEECLRPGVVSDSTFLAKLNQLFSKHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASKDAESPSWRSTTVLGLLDIYGFEVFQHNSFEQFCINYCNEKLQQLFIELTLKSEQEEY 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LGVEGTTLREALTHRKITAKGEELLSPLNLEQAAYARDALAKAVYSRTFTWLVRKINRSL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VGLNSVELERALCSRTMETAKEKVVTTLNVIQAQYARDALAKNIYSRLENWLVNRINESI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VMRKALSVIDFTEDEVEDLLSIVASVLHLGNIHFAADEDSN----AQVTTENQLKYLTRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RVVKQLEGERNFHIFYQLLAGADAQLLKALKLERDTGGYAYL-NPDTSRVDGMDDDANFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RVVHQNHGERNFHVFYQLLEGGEEETLRRLGLERNPQSYLYLVKGQCAKVSSINDKSDWK
                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -KRKVMGVLDIYGFEILEDNSFEQFVINYCNEKLQQVFIEMTLKEEQEEY
                                          32, Created)
40, Last sequence update)
41, Last annotation update)
1 Ialpha) (MMI-alpha) (MMIa)
                                                                                                                                                                     1024
                                                                                                                                                                                           1014
  Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                          1107
                                              (MIH-L)
Murinae;
                                                                                                                                                                                                                                                                                                                                                    -----WK-CK
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Query Match
Best Local S
Matches 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Molecular cloning of a mouse myosin if expressed in brain.";
FEBS Lett. 320:121-124(1993)
-i- FUNCTION: MOTOR PROTEIN THAT MAY PARTICIPATE IN PROCESS CRITO NEURONAL DEVELOPMENT AND FUNCTION SUCH AS CELL MIGRATION NEURITE OUTGROWTH AND VESICULAR TRANSPORT.
-i- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE PRODUCED BY ALTERNATIVE SPLICING.
-i- TISSUE SPECIFICITY: PROMINENT EXPRESSION IS SEEN IN THE BRAIL AND AND TUSTE SPECIFICITY: PROMINENT EXPRESSION IN THE HEART AND TESTIF HIGH LEVEL EXPRESSION IS SEEN IN VIRTUALLY ALL NEURONS (BUTTHE CEREBELLAR EXTERNAL AND ADULT MOUSE BRAIN AND IN NEUROBLIF CEREBELLAR EXTERNAL AND ADULT MOUSE BRAIN AND IN NEUROBLIF SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
-i- SIMILARITY: CONTAINS 5 IQ DOMAINS.
                                                                 CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                         DOMAIN
NP_BIND
                                                                                                                                                                                                                                                      Multigene
DOMAIN
                                                     SEQUENCE
                                                                                                                                                                                                                                                                                   SMART; SM00015; IQ; 5.
SMART; SM00242; MYSC;
PROSITE; PS50096; IQ;
                                                                                                                                                                 VARSPLIC
                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                      PRINTS; PR00193; MYOSINHEAVY. ProDom; PD000355; myosin_head;
                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000048; IO_region.
InterPro; IPR001609; myosin_head.
Pfam; PF00653; myosin_head; 1.
Pfam; PF00612; IO; 5.
                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                              Myosin;
                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P08799; 1MND.
MGD; MGI:107732; Myola.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L00923; EMBL; X69987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C57BL/6; TISSUE=Brain; MEDLINE=93209370; PubMed=8458427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sherr E.H., Joyce M.P., Greene L.A.; "Mammalian myosin I alpha, I beta, a genes of the myosin I family.", Cell Biol. 120:1405-1416(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 13-1107 FROM N.A. (ISOFORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Koslovsky J.S., Qian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=93194946;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-10090;
[1]
        463;
                Similarity
                                                                                                                                                                                                                                                                         ATP-binding; Actin-binding;
                                                                                                                                                                                                                                                             family;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FROM N.A. (ISOFORM 1).
57BL/6; TISSUE=Cerebellum;
                                                     704
728
750
780
808
108
592
791
44
260
304
307
333
307
333
546
570
     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                    AAA39800.1; -. CAA49604.1; -.
                                                     ĀΑ;
                                                                 749
778
807
837
115
599
819
44
260
304
317
317
333
546
571
                                                                                                                                                                                                                                                   Alternative 727
           38.7%;
41.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PubMed-8449986;
                                                    128527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C., Jiang X.,
      183;
                                                         ACTIN BINDING (POTENTIAL).

MISSING (IN ISOFORM 2).

I -> R (IN REF. 2).

I -> Y (IN REF. 2).

N -> I (IN REF. 1).

KEICELTSIDO -> NEKFASRPASVK ()

Q -> R (IN REF. 1).

G -> D (IN REF. 1).

AG -> RS (IN REF. 2).

A -> E (IN REF. 2).
                                                    MW;
                                                                                                                                                                                  ve splicing.
IQ 1.
IQ 2.
IQ 3.
IQ 3.
IQ 4.
IQ 5.
ATP (POTENTIAL).
               Pred. No.
                          Score
   Mismatches
                                                 FA244E5D2DE752A5 CRC64;
                          2090.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and
                                                                                                                                                                                                                                                                      Calmodulin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mercer J.A.;
               5.1e-125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gamma: new widely expressed
                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S SEEN IN THE BRAIN, IE HEART AND TESTIS.
 Indels 119;
                       Length 1107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             γď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IN NEUROBLASTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MIGRATION
                                                                                                                                                                                                                                                                     Repeat;
                                                                                                          (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BRAIN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRITICAL
Gaps
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19;
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1023
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                                            963
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KEGSEAASKGDFLFSSDHLIEMATKLYRTTLSQTKQKLNIEISDEFLVQFRQDKVCVKFI
                                                                                                              PVVKYDRKGYKPRPRQLLLTPSAVVIVE--DAKVKQRIDYANLTGISVSSLSDSLFVLHV
                                                                                                                                                                                                        KQQLQQKAVASEIFKGKKDNYPQSVPRLFISTRLGTEEISP----RVLQSLGSEPIQYAV
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                                      QR-EDNKQKGDVVLQSDHVIETLTK---TALSADRVN-NINI------NQGSITFA 1007
                                                                                   VVNKINRANGKSTSRIFLLTNNNLLLADQKSGQIKSEVPLVDVTKVSMSSQNDGFFAVHL
                                                                                                                                                                      KLIYEEKLEASELFKDKKALYPSSVGQPFQGAYL---EINKNPKYKKLKDAIEEKIIIAE
                                                                                                                                                                                                                                                         IVQKYLLEMKNKMPSLSPIDKNWPSRPYLFLDSTH--KELKRIFHLWRCKKYRDQFTDQQ
                                                                                                                                                                                                                                                                                                      VRASFLLNLRRQLPR-NVLDTSWPTPPPALREASELLRELCMKNMVW----KYCRSISPEW
                                                                                                                                                                                                                                                                                                                                               AYWHGTQARRELKRLKEEARRNDAVAVIWAYWLGLKVRREYRKFFRANAGKKIYEFTLQR
                                                                                                                                                                                                                                                                                                                                                                                                                                    KRSQVVIAAWYRRYAQQKRYQQIKSSALVIQSYIRGWKARKILRELKHQKRCKEAATTIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KRSAICIQSWWRGTLGRRKAAKRKWAAQTIRRLIRGF----ILRHSPRCPENA----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NESLVCHQIRYLGLLENVRVRRAGYAFRQAYEPCLERYKMLCKQTWPHWKGPARSGVEVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EAEGIAWEPVQYFNNKIICDLVEEKFKGIISILDEECLRPGEATDLTFLEKLEDTVKPHP
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16-OCT-2001 (Rel. 4
16-OCT-2001 (Rel. 4
16-OCT-2001 (Rel. 4
                                                                                                                                                      DOMAIN
VARSPLIC
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NP_BIND
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                                                                                                                                                                                                                                                                      DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head;
SMART; SM00115; 10; 6.
SMART; SM00242; MYSC; 1.
PROSITE; PS50996; 10; 5.
                                                                                                       VARSPLIC
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Myosin
                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00063; myosin_head; 1. Pfam; PF00612; IQ; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X68199; HSSP; P08799;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 myosin-I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ruppert C., Kroschewski R., Baehler M. "Identification, characterization and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93194945; PubMed=8449985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=Sprague-Dawley;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Myosin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001609; myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QGNQKNGSVP---
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  463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATP-binding;
                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                     family;
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1136
  Conservative
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40, Last sequence update)
40, Last annotation update)
1 alpha) (MMI-alpha) (MMIa)
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                         38.5%;
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                                                                                                         131917
183;
                                                                                                 IQ 1.
IQ 2.
IQ 3.
IQ 4.
IQ 5.
IQ 6.
ATP (POTENTIAL).
ACTIN-BINDING (POTENTI MISSING (IN ISOFORM 1E MISSING (IN ISOFORM 1C MISSING (IN IS)
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  splicing
  Mismatches
                              2080;
No. 2
                           No.
                                                                                                                                                                                                                                                                                                                                                                                                         HEAD-LIKE
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                                                                                                                                                                                  (POTENTIAL).
  346;
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                                                                                                    ( 1B).
( 1C).
:2 CRC64;
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                                                  Length 1136;
  Indels
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  148;
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               SADRVN-NINI --
                                 GQIKSEVPLVDVTKVSMSSQNDGFFAVHLKEGSEAASKGDFLESSDHLIEMATKLYRTTL 1082
                                                            AKVKQRIDYANLTGISVSSLSDSLFVLHVQR-EDNKQKGDVVLQSDHVIETLTK---TAL 989
                                                                                                         AYL---EINKNPKYKKLKDAIEEKIIIAEVVNKINRANGKSTSRIFLLTNNNLLLADQKS
                                                                                                                                           TRLGTEEISP----RVLQSLGSEPIQYAVPVVKYDRKGYKPRPRQLLLTPSAVVIVE--D
                                                                                                                                                                            DSTH---KELKRIFHLWRCKKYRDQFTDQQKLIYEEKLEASELFKDKKALYPSSVGQPFQG
                                                                                                                                                                                                   EASELLRELCMKNMVW---KYCRSISPEWKQQLQQKAVASEIFKGKKDNYPQSVPRLFIS
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--NQGSITFAGGPGRDGIIDFTSGSELLITKAKNGHLAVVA
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Pfam; PF00612; IQ; 3.
PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head; 1
SMART; SM00015; IQ; 3.
SMART; SM00242; MYSC; 1.
PROSITE; PS50096; IQ; 2.
                                                                                                                                                        Myosin; Ac
Multigene
                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF127026; AAD31189.1; -.
EMBL; AF105424; AAC78645.1; -.
EMBL; AF009961; AAC27437.1; -.
HSSP; P08799; IMND.
Genew; HGNC:7595; MYO1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SEQUENCE FROM N.A.

MEDLINE-99073867; PubMed-9858156;

Skowron J.F., Bement W.M., Mooseker M.S.;

"Human brush border myosin-I and myosin-Ic expression in intestine and Caco-2BBe cells.";

Cell Motil. Cytoskeleton 41:308-324(1998);

Cell Motil. Cytoskeleton 41:308-324(1998);

Cell Motil. Cytoskeleton 41:308-324(1998);
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16-OCT-2001 (Rel. 40, 0
16-OCT-2001 (Rel. 40, 1
16-OCT-2001 (Rel. 40, 1
                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000048; IQ_region.
InterPro; IPR001609; myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACTIN FILAMENTS (POTENTIAL).
-!- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
-!- SIMILARITY: CONTAINS 3 IQ DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Jejunal brush border;
MEDLINE=20119970; PubMed=10653589;
Li W., Wang J., Coluccio L.M., Matsudaira
"Brush border myosin I (BBMI): a basally l
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Intestine;
Bikle D.D., Munson S.J.;
"Human brush border myosin
Submitted (FEB-1999) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           jejunal enterocytes.";
J. Histochem. Cytochem.
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Eukaryota; Metazoa; (
Mammalia; Eutheria; I
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Primates;
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Last sequence update)
Last annotation update)
(BBM-I) (BBMI) (Myosin I heavy chain) (MIHC).
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MYOSIN HEAD-LIKE
IQ 1.
IQ 2.
IQ 3.
ATP (POTENTIAL).
ACTIN-BINDING (P
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                                                                                                                                                                  Calmodulin-binding;
                                                                                                                          HEAD-LIKE
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localized transcript in
(POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                             SMNPIMAQCEDKS--ELSDKKRPETVATQFKMSLLQLVEILRSKEPAYIRCIKPNDAKQP 615
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                                                                                | CLSPKQVEILREKLCASELFKGKKASYPQSVPIPFCGDYIGLQG-NPKLQKLKGGEEGPV
                                                                                                                                                                                                                                                                  AVLVRHLGYKPEEYKMGRTKIFIRFPKTLFATEDSLEVRRQSLATKIQAAWRGFHWRQKF 735
                                                                                                                                                                                                                                                                                                                                                              AQHPLLRSLFPEGNPKQASLKRPPTAGAQFKSSVAILMKNLYSKSPNYIRCIKPNEHQQR 597
                                                                                                                                                                                                                                                                                                                                                                                                                    GHY--ESKVTQNAQRQYDHTMGLSCFRICHYAGKVTYNVTSFIDKNNDLLFRDLLQAMWK 537
                                                                                                                                                                                                                                                                                                                                                                                                                                   PHFLTHKLADQKTRKSLDR-----GEFRLLHYAGEVTYSVTGFLDKNNDLLFRNLKETMCS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LASKDAESPSWRSTTVLGLLDIYGFEVFQHNSFEQFCINYCNEKLQQLFIELTLKSEQEE 441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MVGLNSEEVERALCSRTMETAKEKVVTALNVMQAQYARDALAKNIYSRLFDWIVNRINES
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                                               QYAVPVVKYDRKGYKPRPRQLLLTPSAVVIVEDAKVKQR--IDYANLTGISVSSLSDSLF
                                                                                                            SISPEWKQQLQQKAVASEIFKGKKDNYPQSVPRLFISTRLGTEEISPRVLQSLGSE--PI
                                                                                                                                      {\tt FIYKSMVQKFLLGLKNNLPSTNVLDKTWPAAPYKCLSTANQELQQLFYQ---wKCKRFRD}
                                                                                                                                                                HVRAS----FILNLRRQLP-RNVLDTSWPTPP-PALREASELLRELCMKNMVWKYCR---
                                                                                                                                                                                             QLMRKSQILISSWFRGNMQKKCYGKIKASVLLIQAFVRGWKARKNYRKYFRSEAALTLAD
                                                                                                                                                                                                                      LRVKRSAICIOSWWRGTLGRRKAAKRKWAAQTIRRLIRGFILRHSPR----CPENAFFL-D
                                                                                                                                                                                                                                                  EKVLGELSMSSGELAFGKTKIFIRSPKTLFYLEEQRRLRLQQLATLIQKIYRGWRCRTHY
                                                                                                                                                                                                                                                                                                        GQFSSDLVATQARYLGLLENVRVRRAGYAHRQGYGPFLERYRLLSRSTWPHWNGGDREGV
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                            LMAEAVKKVNRGNGKTSSRILLLTKGHVILTDTKKSQAKIVIGLDNVAGVSVTSLKDGLF
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1043
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712
118400
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Pred. No. 2.1
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> G (IN REF. 3).
EE5D79D9D6E085DC
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RESULT 8
MYHL_CHICK
ID H_VHL_CA
AC P47807
DT 01-FEB
DT 11-OCT
RAT GAILUS
OC Archos
RAT GAILUS
RAT GAICL
RA
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MEDLINE-97148341; PubMed-8994973;
HOUGUSSE A., Silver M., Cohen C.;
"A model of Ca(2+)-free calmodulin binding to unconventional reveals how calmodulin acts as a regulatory switch.";
Structure 4:1475-1490(1996).
-!- FUNCTION: COULD PLAY AN IMPORTANT ROLE IN MORPHOGENESIS & FUNCTION OF INTESTINAL MICROVILLI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mooseker M., Louvard D., Arpin M.;
"Partial deduced sequence of the 110-kD-calmodulin avian intestinal microvillus shows that this mechan member of the myosin I family.",
J. Cell Biol. 109:2895-2903(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WYHL_CHICK STANDARD; PRT; 1045 AA.
P47807; Q90573;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Brush border myosin I (BBM-I) (BBMI) (Myosin I heavy chain) (MIHC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                             DOMAIN
DOMAIN
                                                                                                                                     ProDom; PD000355; myosin_head;
SMART; SM00015; IQ; 5.
SMART; SM00242; MYSC; 1.
PROSITE; PS50096; IQ; 3.
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                                                                                                                                                                                                                   Pfam; PF00063; myosin_head; 1.
Pfam; PF00612; IQ; 3.
PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head;
                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U04049; AAB38373.1; -. EMBL; X58479; CAA41388.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Intestine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Collins K., Matsudaira P.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=96114119; PubMed=8681398;
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                                                                                    Myosin; Actin-binding; ATP-binding; Calmodulin-binding; Multigene family; 3D-structure.
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PDB; 1AJI; 17-SEP-9
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  DOMAIN
                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000048; IQ_region.
InterPro; IPR001609; myosin_head.
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                                                            family;
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  701
723
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Neognathae; Galliformes; Phasianidae; Phasiani
MYOSIN
IQ 1.
IQ 2.
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                                                            HEAD-LIKE
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              KYCRSISPEWKQQLQQKAVASEIFKGKKDNYPQSVPRLFISTRLG-TEEISPRVLQSLGS
                                          ACTRLSNFTYRRMVQKYLMGLQKNLPPMAVLDRTWPPAPYKFLSDANQELKSTFYRWKCK
                                                       WCCRKRYQLMRKSQILISAWFRGHMQRNRYKQMKRSVLLLQAYARGWKTRRMYRRYFRSD
                                                                                                          FHWRQKFLRVKRSAICIOSWWRGTLGRRKAAKRKWAAQTIRRLIRGFILR------HSP
                                                                                                                                  GGDREGAEVLLAELKEPPEELAYGHTKIFIRSPRTLEDLEKRRQQRVAELATLIQKMERG
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%; Pred. No. 1.2e-:
197; Mismatches :
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ATP (OTENTIAL).

ACTIN-BINDING (POTENTIAL).

ACTIN-BINDING (POTENTIAL).

E -> Q (IN REF. 2).

C -> S (IN REF. 2).

T -> A (IN REF. 2).

G -> A (IN REF. 2).

CASE -> WPRQ (IN REF. ...).
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375;
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RESULT 9

WYHL_MOUSE

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Query Match
Best Local Similarity
                                                                               NON_TER
SEQUENCE
                                                                                                                            DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                Myosin; Actin-binding; ATP-binding; Calmodulin-binding;
Multigene family.
                                                                                                                                                                                                                                                                                                                             SMART; SM00015; IQ; 3.
SMART; SM00242; MYSC; 1.
PROSITE; PS50096; IQ; 2.
                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000048; IQ_region.
InterPro; IPR001609; myosin_head.
Pfam; PF00063; myosin_head; 1.
Pfam; PF00612; IQ; 3.
PRINTS; PR00193; MYOSINHEAVY.
PRODOM; PD000355; myosin_head; 1.
SMARF. SMARF. 50001515.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGD; MGI:1338019; Myhl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and embryonic intestine.";
J. Exp. Zool. 283:242-257(1999).
-!- FUNCTION: INVOLVED IN DIRECTING THE ACTIN FILAMENTS (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Skowron J.F., Mooseker M.S.; "Cloning and characterization of mouse brush border myosin-I in and ambryonic intestine.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF009960; AAC28397.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=99132700; PubMed=9933937;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Brush border myosin I (BBM-I) (BBMI) (Myosin I heavy chain) (MIHC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Fragment).
MYHL OR BBM-I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DVAVTVVESAKGGGDVPVCKKRGSH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DKLVMAEAVQKVNRANGKTVPRLLLLTTEHLVLADPKAAQPKMVLSLCDIQGASVSRFSD
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                                                                                                                                                                                                                                                                             family.
                                                                               AA;
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44.8%;
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Rodentia; Sciurognathi; Muridae;
                                                                          MW;
                                                                                                                    MYOSIN HEAD-LI
IQ 1.
IQ 2.
IQ 3.
ATP (BY SIMILA
ACTIN-BINDING
  Score
Pred.
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1987; DB 1;
No. 1.4e-118;
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Euteleostomi;
; Murinae; Rat

Rattus

DOMAIN

testis.";

ALONG

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RESULT 10
MYHL_RAT
ID MYHL_
AC Q6277
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DT 16-OC
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                                                                                                            TVKKVNR
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                                                                                                                                     PVVKYDR
                                                                                                                                                                                                                                  QMRKSQILISAWFRGNKQKKHYGKIRSSVLLIQAFVRGWRARKNYRKYFRSGAALTLANF
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                                                                                                                                                                KQVQTLREKLCASELFKGKKASYPQSVPIPFRGDYIGLQG-NPKLQRLKGREEGPVLVAD
                                                                                                                                                                                        EWKQQLQQKAVASEIFKGKKDNYPQSVPRLFISTRLGTEEISPRVLQSLGSE--PIQYAV 904
                                                                                                                                                                                                                    IYQSMAQKFLLNLKKNLPSTKVLDNTWPAAPYRCFNTANQELQRLFYQWKCKKFRDQLSP
                                                                                                                                                                                                                                                                                                  RVKRSAICIQSWWRGTLGRRKAAKRKWAAQTIRRLIRGFILRHSPRCPENA-----F
                                                                                                                                                                                                                                                                                                                                                      VLVRHLGYKPEEYKMGRTKIFIRFPKTLFATEDSLEVRRQSLATKIQAAWRGFHWRQKFL 736
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(Rel.
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                                                                                                                                     911
                                          STANDARD;
40,
 Last sequence update)
               Created)
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                                          842
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Matches 388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00015; IQ; 3. SMART; SM00242; MYSC; 1. PROSITE; PS50096; IQ; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00063; myosin_head; 1.
Pfam; PF00612; IQ; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Identification of brush border myosin-I in liver and testis.", Biochem. Biophys. Res. Commun. 211:331-339(1995).
-!- FUNCTION: INVOLVED IN DIRECTING THE MOVEMENT OF ORGANELLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Sprague-Dawley; TISSUE=Liver, MEDLINE=95298044; PubMed=7779104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Last annotation update)
Brush border myosin I (BBM-I) (BBMI) (Myosin I heavy chain) (MIHC)
                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00193; MYOSINHEAVY. ProDom; PD000355; myosin_head;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000048; IQ_region.
InterPro; IPR001609; myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTIN FILAMENTS (POTENTIAL).
-!- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD
-!- SIMILARITY: CONTAINS 3 IQ DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Balish M.F., Coluccio L.M.;
"Identification of brush border
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MYHL OR BBMI.
                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Myosin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P08799;
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               239
                                        268
                                                                   180
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                                                                                                                     MRKALSVIDFTEDEVEDLLSIVASVLHLGNIHFAADEDSN----AQVTTENQLKYLTRLL
                                                                                                                                                                           VSFYEVPPHLFAVADTVYRALRTERRDQAVMISGESGAGKTEATKRLLQFYAETCPAPER 147
              VQNAMAVIGFSEEEIRQVLEVTALVLKLGNVKLAGEFQANGLPASGVCDGKGIQEIGEMM
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Actin-binding;
                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                      family.
                                                                                                                                                                                                                                                                                                                                           842
                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                       673
712
733
764
842
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                                                                                                                                                                                                                                                                                                  35.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATP-binding; Calmodulin-binding;
                                                                                                                                                                                                                                                                                     165;
                                                                                                                                                                                                                                                                                                                                                                   MYOSIN
IQ 1.
IQ 2.
IQ 3.
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                                                                                                                                                                                                                                                                                                               Score 1932.5;
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                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                             HEAD-LIKE
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16-OCT-2001 (Rel. 40, Last sequence upda
15-JUN-2002 (Rel. 41, Last annotation up
Myosin IA (MIA) (Brush border myosin IA)
MYO31DF OR CG7438.
Drosophila melanogaster (Fruit fly).
Eukaryota: Metazoa: Arthropoda; Mandalbul
MEDLIND-2019606; PubMed-10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashbuxner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.
                                                                                                                     STRAIN-Berkeley;
                                                                                                                                                                                Morgan N.S., Skovronsky D.M., Artavanis-Tsakonas S., Mooseker M.S. "The molecular cloning and characterization of Drosophila melanoga myosin-IA and myosin-IB.";
                                                                                                                                                                                                                              TISSUE~Embryo;
MEDLINE-94260541; PubMed-8201616;
                                                                                                                                                                                                                                                                                              Insecta: Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta: Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.,
                                                                                                                                      SEQUENCE FROM N.A.
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Q23978;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FTSELVMVQARYLGLLENVRVRRAGYAFRQAYKPFLERYRLLSRSTWPRWNGEDREGVEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGIPWTKVEYFDNGIICDLIEHSQRGILAMLDEECLRPGVVSDTTFLAKLNQLFSKHSH
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                                                                                                                                                                      Biol.
                                                                                                                                                                 and myosin-ĬB.";
iol. 239:347-356(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                            update)
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Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA

Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA

ROTER D. Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA

Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA

Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies R.,

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Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

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Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

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RA

Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dleitz S.M.,

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Fosler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA

RA

Hostin M., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,

RA

RA

Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA

Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,

RA

Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA

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Rainert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

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Rainert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA

Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,

RA

RA

Rainert K., Remington C., Turner R., Venter E., Wang A.H., Wang X.,

RA

RA

Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,

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RA

Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

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Spier B., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

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Spier S., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

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Spier S., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

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Spier S., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA

Spier S.
                                                                                                                                                                                                                                                                                                                                                            Morgan N.S., Heintzelman M.B., Mooseker M.S., "Characterization of myosin-IA and myosin-IB, myosins associated with the Drosophila brush
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=96069904; PubMed=7589814;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION,
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Ballew R.M., Basu A., Baxendale
Beeson K.Y., Benos P.V., Bernan
Beeson K.Y., Benos P.V., Bernan
                                                                                                                               BIOL 172:51-71(1995).

FUNCTION: INVOLVED IN DIRECTING THE MOVEMENT OF ORGANELLES ACTIN FILAMENTS (BY SIMILARITY).

SUBCELLULAR LOCATION: CYTOPLASMIC. PROTEIN SHIFTS FROM THE BASOLATERAL TO APICAL DOMAIN IN ENTEROCYTES AND FOLLICLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     An H.-J., Andrews-Pfannkoch C.,
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                                                                                                                                                                                                                                                                                                                                                                      border cytoskeletor
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                                                                                                                                                                                                                                                                                                                                                                      cytoskeleton.";
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MIDGUT CELLS OF THE PROVENTRICULUS, AND IN THE MID AND HINDGUT. I
THE LARVAL GUT BRUSH BORDER, EXPRESSION IS IN THE TERMINAL WEB
DOMAIN. IN THE ADULT GUT BRUSH BORDER, EXPRESSION IS IN THE TERMINAL WEB
DOMAIN. IN THE ADULT GUT BRUSH BORDER, EXPRESSION REMAINS IN THE
WEB DOMAIN AND HAS ALSO MOVED INTO THE MICROVILLI. ALSO EXPRESSED
AT LOW LEVELS IN FOLLICLE CELLS DURRING OCCENESIS.
DEVELOPMENTAL STAGE: EXPRESSED BOTH MATERNALLY AND ZYGOTICALLY
THROUGHOUT DEVELOPMENT TO ADULTHOOD WITH HIGHEST LEVELS AT THE EN
OF LARVAL DEVELOPMENT. EXPRESSION IN EMBRYOGENESIS IS CORRELATED
WITH THE FORMATION OF A BRUSH BORDER WITHIN THE ALIMENTARY

SIMILARITY: SIMILARITY: CONTAINS 2 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN. IQ DOMAINS.

EMBL; EMBL; HSSP; entities or send a FlyBase; FBgn0011673; Myo31DF use by non-profit institutions as long modified and this statement is not removed use s SWISS-PROT entry is copyright. It ween the Swiss Institute of Bioinformatics Institute. P08799; U07595; AAA19590.1; AE003628; an requires IPR000048; equires a license agreement (seemail to license@isb-sib.ch). AAF52966.1; Bioinformatics It is produced through (See There are no as http://www Usage its content and the restrictions tent is in .isb-sib.ch/announce/ EMBL ಬ for collaboration пo

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SMART; SM00242; MYSC; 1.
PROSITE; PS50096; IQ; 1.
Myosin; ATP-binding; Actin-binding; Calmodulin-binding;
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NP_BIND
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RASFLLNLRRQL--PRNVLD----TSWPTPPPALREASELLR---ELCMKNMV-WKYCRS
                                                                                                                             STVFDEERVEHQVRYLGLLENLRVRRAGFVHRQRYDKFLLRYKMISQYTWPNFRAGSDRD
                                                                                                                                                                                  NLSEMWPEGAQDIKKT----TKRPLTAGTLFQRSMADLVVTLLKKEPFYVRCIKPNDLKS
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                                                  KFLRVKRSAICIQSWWRGTLGRRKAAKRKWAAQTIRRLIRGFILRHSPRCPENAFFLDHV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  426;
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Pred. No. 1.2e-106;
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IQ 2.
ATP (BY SIMILARITY)
                        -----AAITIVRAYKAYKLR------
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RESULT 12

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                       Pfam; PF00063; myosin_head; 1.
Pfam; PF00612; IQ; 2.
PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head; 1
SMART; SM00015; IQ; 1.
SMART; SM00015; IQ; 1.
SMART; SM00042; MYSG; 1.
PROSITE; PS50096; IQ; 2.
MYOSIN; Actin_binding; ATP-bindi
Multigene family.
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01-FEB-1994 (Rel. 28, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Myosin IE heavy chain.
MYOE OR DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MYSE_DICDI
Q03479;
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Dictyostelium discoideum (Slime mold).

Dictyostelium discoideum (Slime mold).
                                                                                                                                                                                                                                                                             PIR; $33760; $33760.
HSSP; P08799; IMND.
DictyDb; DD01049; myoE.
InterPro; IPR000048; IQ_region.
InterPro; IPR001609; myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Urrutia R., Jung G., Hammer J.A. III; "The Dictyostellum myosin IE heavy chain gene encodes isoform that lacks sequences corresponding to the acti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biochim. Biophys. Acta 1173:225-229(1993).
-i- FUNCTION: MYOSIN IS A PROTEIN THAT BINDS
ACTIVITY THAT IS ACTIVATED BY ACTIN. MAY
                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L06805; AAA33201.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBUNIT: MYOSIN I HEAVY CHAIN IS SINGLE-HEADED. DIM
AND A LIGHT CHAIN. INABILITY TO SELF-ASSEMBLE INTO
-!- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DO
-!- SIMILARITY: CONTAINS 2 IQ DOMAINS.
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  DOMAIN
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                                                  ATP-binding; Calmodulin-binding;
  MYOSIN HEAD-LIKE
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                     ONHMROKVMAYDIFHCKKKWDFRRHFDADYLEKPWNPNQQKYVLAMQNLF--
                                               KQQLQQKAVASETFKGKK---
                                                                                         DHVRASFLLNLRRQLPRNVLDTSWPTPPPALREASELLRELCMKNMVWKYCRSISP--EW
                                                                                                                                   ROKFLRVKRSAICIOSWWRGTLGRRKAAKRKWAAQTIRRLIRGF-ILRHSPRCPENAFFL
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                                                                  -WPKDPSILDRAVQLTHKI----HNCWRAEKMILSLGAG
                                                                                                                -RSYRYNKW----FRELHRAFKDVARDPQWGKQVF--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1739; DB 1;
Pred. No. 9.5e*103;
1; Mismatches 328;
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MW; B6E758BEC035766F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IQ 1.
IQ 2.
NON ALPHA-HELICAL, C-TERMINAL DOMAIN.
ATP (BY SIMILARITY).
ACTIN-BINDING.
                                             DNYPQSVPRLFISTRLGTEEI
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SMART;

", SM00015; IQ; 1.", SM00242; MYSC; 1.", SM00326; SH3; 1.", PS50096; IQ; 1.", TE; PS50002; SH3; 1."

PRINTS; PR00193; MYOSINHEAVY.
PRINTS; PR00452; SH3DOMAIN.
Probom; PD000066; SH3; 1.
Probom; PD000355; myosin\_head;

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RESULT 13

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hamel C., Fizames C., Levi-Acobas F., Depetris D., Mattei M.-G.,
Weil D., Pujol R., Petit C.;
"Cloning of the genes encoding two murine and human cochlear
unconventional type I myosins.";
Genomics 40.332-341(1997).

-i-FUNCTION: MYOSINS ARE ACTIN-BASED MOTOR MOLECULES WITH ATPASE
ACTIVITY. UNCONVENTIONAL MYOSINS SERVE IN INTERCELLULAR MOVEMENTS.
THEIR HIGHLY DIVERGENT TAILS ARE PRESUMED TO BIND TO MEMBRANOUS
COMPARTMENTS, WHICH WOULD BE MOVED RELATIVE TO ACTIN FILAMENTS (BY
SIMILARITY).

-i-TISSUE SPECIFICITY: EXPRESSED IN LIVER, KIDNEY, SPLEEN, EYE,
BRAIN, LUNG, SMALL INTESTINE, TESTIS AND COCHLEA. BARELY
                                                                                                                                                                                                                                    Pfam; PF00063; myosin_head; 1. Pfam; PF00612; IQ; 1.
                                                                                                                                                                                                                                                                                       Pfam; PF00018; SH3; 1
                                                                                                                                                                                                                                                                                                       InterPro: IPR000048; IQ_region.
InterPro: IPR001452; SH3.
InterPro: IPR001609; myosin_head.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement ( or send an email to license@isb-sib.ch)
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16-0CT-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DETECTABLE IN HEART.
SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
SIMILARITY: CONTAINS 1 IQ DOMAIN.
SIMILARITY: CONTAINS 1 SH3 DOMAIN.
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Rodentia;
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Sciurognathi;
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Depetris D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       AEGIAWEPVQYFNNKIICDLVEEKFK--GIISILDEECL---RPGEATDLTFLEKLEDTV 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QKPQEEYS-----IGVLDIYGFEIFQKNGFEQFCINFVNEKLQQIFIELTLKAEQEEYV 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GRLQEKLTSRKMDSKWGGRSESIDVTLNVEQAAYTRDALAKGLYARLFDFLVEAINRAM- 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TLSAMQVMGFRQACQQLVLQLVAGILHLGNISF-CEEGNYARVESVDSLAFPAYLLGIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VVHQNHGERNFHVFYQLLEGGEEETLRRLGLERNPQSYLYLVKGQCAKVSSINDKSDWKV 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VSFYEVPPHLFAVADTVYRALRTERRDQAVMISGESGAGKTEATKRLLQFYAETCPAPER 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GVDDMVLLSQIT-EDAIVRNLHKRFMDDYIFTYIGSVLISVNPFKQMPYFTDREIDLYQG 76
               ASEIFKGKKDNYPQSVPRLFISTRLGTEEISPRVLQSLGS-EPIQYAVPVVKYDRKGYKP 916
                                                                                                                                                                                                                                                         FDEVLIRHQVKYLGLMENLRVRRAGFAYRRKYEAFLQRYKSLCPETWPMWAGRPQDGVAV 677
                                                                                                                                                                                                                                                                                                                                  MNPIMAQCF-DKSELSDKKRPETVATQFKMSLLQLVEILRSKEPAYIRCIKPNDAKQPGR 617
                                                                                                                                                                                                                                                                                                                                                                  GTHEHF-----NSWSAG-FVIHHYAGKVSYDVSGFCERNRDVLFSDLIELMQSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SKDAESPSWRSTTVLGLLDIYGFEVFQHNSFEQFCINYCNEKLQQLFIELTLKSEQEEYE 443
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ASNILLNKKERRRNSINRNFVGNYLGLEE-RPELRQFLAKRERVDFADSVTKYDRR-FKP
                                                                                                                                                                                LLRAVNMEPDQYQMGSTKVFVKNPESLFLLEEMRERKFDGFARTIQKAW----
                                                                                                                                                                                                              LVRHLGYKPEEYKMGRTKIFIRFPKTLFATEDSLEVRRQSLATKIQAAWRGFHWRQKFLR 737
                                                                                                                                                                                                                                         WEESRVKHQVEYLGLRENIRVRRAGFAYRRQFSKFLQRYAILTPETWPRWRGDERQGVQH 655
                                                                                                                                                                                                                                                                                                                                                                                                                            QEGIRWTPIEYFNNKIVCDLIENKLSPPGIMSVLDDVCATMHATGGGADQTLLQKLQAAV 487
                                                                                    LLNLRRQLPRNVLDTSWPTPPPALREASELLRELCMKNMVWKYCRSISPEWKQQLQQKAV 857
                                                                                                                                                  VKRSAICIQSWWRGTLGRRKAAKRKWAAQTIRRLIRGFILRHSPRCPENAFFLDHVRASF 797
                                                                                                                                                                                                                                                                                                     DQDFLRMLFPEKLNIDKKGRPSTAGSKIKKQANDLVSTLKKCTPHYIRCIKPNETKRPRD
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9; Mismatches 297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1726.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            1SOFORM. 7,

1SOFORM. 7,

1J. BIOL. Chem. 268:14981-14990(1993).

1J. BIOL. Chem. 268:14981-14990(1993).

1-FUNCTION: MYOSIN IS A PROTEIN THAT BINDS TO ACTIN & HAS ATPASE ACTIVITY THAT IS ACTIVATED BY ACTIN. MYOSIN IB MAY HAVE A ROLE IN CHEMOTAXIS AND AGGREGATION; IT COULD SERVE TO STABILIZE AND EVEN RETRACT CORTICAL STRUCTURES, SUCH AS SESUDOPODS AND LAMELLOPODS.

1- SUBGUNIT: MYOSIN I HEAVY CHAIN IS SINGLE-HEADED. DIMER OF A HEAVY AND A LIGHT CHAIN. INABILITY TO SELF-ASSEMBLE INTO FILAMENTS.

1- SUBCELLULAR LOCATION: HIGHEST CONCENTRATION JUST BENEATH THE PLASMA MEMBRANE IN THE ANTERIOR PSEUDOPOD AT THE LEADING EDGE OF
            HSSP; P08799; 1MND. DictyDb; DD01047; myc InterPro; IPR000048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WEDLINE=933194/5; Fubreco-volume G., Fukui Y., Martin B., Hanmer J.A. III;
"Sequence, expression pattern, intracellular localization, and
"Sequence, expression of the nictocatelium myosin ID heavy chain
                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Myosin IB heavy chain. MYOA OR DMIB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P34092;
01-FEB-1994
                                                                                                                                      or send an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Mycetozoa; NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MYSB_DICDI
                                                                          PIR; A33284; A33284.
                                                                                              EMBL; M26037; AAA33229.1;
                                                                                                                                                          entities requires a
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                                                                                                                                                                                                                                                                                    THE CELL.

THE OBLI.

DOMAIN: TH.1 BINDS DIRECTLY TO ANIONIC PHOSPHOLIPID MEMBRANES;

MYCSINS I COULD THEREFORE MOVE ACTIN RELATIVE TO MEMBRANES AND

WICE VERSA. TH.2 AND SH3 BIND TIGHTLY TO F-ACTIN; THIS TOGETHER

WITH THE NUCLECTIDE-SENSITIVE SITE IN THE HEAD, ALLOWS SINGLE

MOLECULES OF MYOSIN I TO CROSS-LIAN ACTIN FILAMENTS.

SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.

SIMILARITY: CONTAINS 1 SH3 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGTRN--VTFSAGQVNLAVLKAGGKTLTI 913
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IKRDLILTPKCVYVIGTEKVKRGPEKGLVREVLKKKLDIQALRGVSLSTRQDDFFIL--Q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REDNKQKGDVVLQSDHVIETLTKT---ALSADRVNNININQGSITF------A 1007
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saxe C.L. III, Kimmel A.R.,
IPR000048; IQ_region IPR001452; SH3.
                                                                                                                                 equires a license agreement (See http://www.isb-sib.ch/announce/email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Acad. Sci. U.S.A. 86:6186-6190(1989)
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                                     myoA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           656-666 AND 783-798
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InterPro;

IPR001609;

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SEQUENCE
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DOMAIN
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Myosin; Actin-binding; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR00193; MYOSINHEAVY.
PRINTS; PR00452; SH3DOMAIN.
ProDom; PD000066; SH3; 1.
ProDom; PD000355; myosin_head;
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         RPQDGVAVLVRHLGYKPEEYKMGRTKIFIRFPKTLFATEDSLEVRRQSLATKIQAAWRGF
                                 GVQDFVLLENETSEAAFIENLRRRFRENLIYTYIGPVLVSVNPYRDLQIYSRQHMERYRG
                                                                               AIQCSKMPFLASLFNEDTGSLQKKRPTTAGFKIKTSAGELMKALSQCTPHYIRCIKPNET
                                                                                                     TMCSSMNPIMAQCEDKSELS-DKKRPETVATQEKMSLLQLVEILRSKEPAYIRCIKPNDA
                                                                                                                               GIYDGHLHWRGMT
                                                                                                                                                   DTVKPHPHF---LTHKLADQKTRKSLDRGEFRLLHYAGEVTYSVTGFLDKNNDLLFRNLKE
                                                                                                                                                                                      EEYEAEGIAWEPVQYFNNKIICDLVEEKF-KGIISILDEECL---RDGEATDLTFLEKLE
                                                                                                                                                                                                                       QSLSY--YKSP---YQNVIGILDIFGFEIFEKNGFEQFCINFVNEKLQQFFIELTLKAEQ
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                                                                                                                                                                                                                                                                                                                                                                                       VVHQNHGERNFHVFYQLLEGGEEETLRRLGLERNPQSYLYLVKGQCAKVSSINDKSDWKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTDDLVMLPK-VSEDEICENLKKRYMNDFIYTNIGPVLISVNPFRNLNNSGPDFIEAYRG
                                                                                                                                                                                                                                                                      ATLQNAILFRVINTGGAGGAGNRRSTYNVPQNVEQANGTRDALARTIYDRMFSWLVEKVN
                                                                                                                                                                                                                                                                                                                     VRQAMDTIGLTAQEQSDIIRIVACVLHIGNIYFIEDDKGNAAIYDPNALELAASMLCIDS
                                                                                                                                                                                                                                                                                                                                           MRKALSVIDFTEDEVEDLLSIVASVLHLGNIHFAADEDSNAQVTTENQLKYLTRLLGVEG
                                                                                                                                                                                                                                                                                                                                                                                                               VEYVKHVILESNPLLEAFGNAKTLRNNNSSRFGKYFEIQFDKAGDPVGGKIYNYLLEKSR
                                                                                                                                                                                                                                                                                                                                                                                                                              EEYVREGIKWEPIKYFNNQIVCDLIEGKSPPGIFSLLDDICSTLHAQSTGTDQKFLEKMA
                                                                                                                                                                                                                                                                                                                                                                  VVYQNPGERNFHIFYQLLRGASAQEKRDYVLS-SPESYYYLNQSQCYTVDGINDVSDYAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                             KHAQEVPPHVYQLAESAYRAMKNDQENQCVIISGESGAGKTEAAKLIMGYVSAISGSTEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF00612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          384;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SM00326; SH3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SM00242; MYSC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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922
1053
102
547
951
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172;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1692.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GLY/PRO/ALA-RICH SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MYOSIN HEAD-LIKE.
TAIL HOMOLOGY REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTIN-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PHOSPHORYLATION (BY SIMILARITY).
                                                                                                                             -GAFAIKHYAGEVTYEAEGFSDKNKDTLFFDLIE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ed. No. 9.96
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ).9e-100;
nes 312;
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2)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        187;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MYSD_DICDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 15
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J. Biol. Chem. 268:14981-14990(1993).

J. BIOL. CHEM. MYOSIN I BAY HAVE A ROLE I CHEMOTAXIS AND AGGREGATION; IT COULD SERVE TO STABILIZE AND EVEN RETRACT CORTICAL STRUCTURES, SUCH AS PSEUDOPODS AND LAWELLOPODS.

J. SUBUNIT: MYOSIN I HEAVY CHAIN IS SINGLE-HEADED. DIMER OF A HEAVY AND A LIGHT CHAIN. INABILITY TO SELF-ASSEMBLE INTO FILAMENTS.

J. SUBCELLULAR LOCATION: HIGHEST CONCENTRATION JUST BENEATH THE PLASMA MEMBRANE IN THE ANTERIOR PSEUDOPOD AT THE LEADING EDGE OF
                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restricted the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dictyostelium discoideum (Slime mold) Eukaryota; Mycetozoa; Dictyosteliida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=93315475; PubMed=8325874;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MYOD OR DMID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Myosin ID heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MYSD_DICDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'Sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             884
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                                                                                                                                               THE CELL.

DOMAIN: TH.1 BINDS DIRECTLY TO ANIONIC PHOSPHOLIDID MEMBRANES;
MYOSINS I COULD THEREFORE MOVE ACTIN RELATIVE TO MEMBRANES AND
VICE VERSA, TH.2 AND SH3 BIND TIGHTLY TO F-ACTIN; THIS TOGETHE
WITH THE NUCLEOTIDE-SENSITIVE SITE IN THE HEAD, ALLOWS SINGLE
MOLECULES OF MYOSIN I TO CROSS-LINK ACTIN FILAMENTS.
SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
SIMILARITY: CONTAINS 1 SH3 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KE--ISFQKSEQCPTLVVKKGGKGLIGTIASGLPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RDGIIDFTSGSE---LLITKAKNGHLAVVAPRLNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VFHLPEHDQVIENDKKTEIIIVLVEYFKAIGGGSLNVQFSDRIN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VLHVQRED----NKQKGDVVLQSDHVIETLTKTALS---ADRVNNININQGSITFAGGPG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VKYDRKGYKPRPRQLLLTPSAVVIVEDAKVK-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HWRQKFLRVKRSAICIQSWWRGTLGRRKAAKRKWAAQTIRRLIRGFILRHSPRCPENAFF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ., Fukui Y., Martin B., Hammer J.A. III; nce, expression pattern, intracellular localization, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          disruption of the Dictyostelium myosin ID heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       604-610; 733-742 AND 914-928
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MBL outstation -
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TOGETHER
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Best Local
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InterPro; IPR001452; SH3.
InterPro; IPR001609; myosin_head.
InterPro; IPR001609; myosin_head.
Pfam; PF00018; SH3; 1.
Pfam; PF00018; SH3; 1.
Pfam; PF00063; myosin_head; 1.
PRINTS; PR00193; myosin_head; 1.
PRINTS; PR00193; myosin_head; 1.
PRODOm; PD000066; SH3; 1.
ProDom; PD000055; myosin_head; 1.
SMART; SM00242; MYSC; 1.
SMART; SM00242; MYSC; 1.
SMART; SM00326; SH3; 1.
PROSITE; PS50002; SH3; 1.
PROSITE; PS50002; SH3; 1.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Multigene family.
                                                                                                                                           421
                                                                                                                                                                                                              378
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           GREDEVLIRHQVKYLGLMENL----RVRRAGFAYRRKYEAFLQRYKSLCPETWPMWAGRP
                                                                                                                                                                                                                                                                                                                                                                             GVQDFVLLENFTSEAAFIENLRRRFRENLIYTYIGPVLVSVNPYRDLQ-IYSRQHMERYR 86
                                           VEGTTLREALTHRKI-----IAKGEELLSPLNLEQAAYARDALAKAVYSRTFTWLVRK 377
                                                                                                                                                                                                                                                                                                VMRKALSVIDFTEDEVEDLLSIVASVLHLGNIHFAADEDSNAQVTTENQ--LKYLTRLLG : ||: || : ::: |: |: :: |:
                                                                                                                                                                                                                                                                                                                                                                                                                           GVSFYEVPPHLFAVADTVYRALRTERRDQAVMISGESGAGKTEATKRLLQFYAETCPAPE 146
| ||:||| :||: | : | 1:||:||||||| | ::|: |
| GKFRYELPPHAYAVADDMYRSMYAEGQSQCVIISGESGAGKTEAAKLIMQYIAAVSGKGA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SFSSHAHF-----QSAAQS-:SSSFTIKHYAGDVEYCAEGFVDKNKDLLENDLVELAA
                                                                                                        VNSALGYKONS-----QSLMIGILDIYGFEIFEKNGFEQMVINYVNERLQQIFIELTLKT
                                                                                                                                                                                                                                                                                  DVCKAMKVIGLTDSEQKEVFRLVAAILYLGNVGFKNNAKDEAAIDQQSKKALENFAFLMQ 305
                                                                                                                                                                                                                                                                                                                                              RVVHQNHGERNFHVFYQLLEGGEEETLRRLGLERNPQSYLYLVKGQCAKVSSINDKSDWK 266
NDFDTSLVMHQVKYLGLLENVRIFGRIRRAGYAYRQTYDKFFYRYRVCCKETWPNWTGGF
                                                                                                                                                                                                                                      TDVSSCEKALCFRTISTGTQGRSARVSTYACPQNSEGAYYSRDALAKALYSRLFDWIVGR
                                                                                                                                                                                                                                                                                                                                 RVVYQTKGERNFHIFYQLLSGANQQLKSELRLD-TPDKFNYLSASGCYTVDGVDDSGEFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tch 29.7%; Score 1601; DB 1; Length 1113; al Similarity 35.8%; Pred. No. 6.5e-94; 372; Conservative 177; Mismatches 301; Indels 188;
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ALA/GLY/PRO-RICH.
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GLY/PRO/ALA-RICH (TH.2).
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TAIL HOMOLOGY REGION 1 (TH.1).
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                                                                   615
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Db	Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy
884	1008	835	956	776	911	729	852	708	792	698	732	651	672
884 ASKQGGKGKERIILFEKG 901	GGPGRDGIIDFTSG 1021	GEVVLKRMNEHDQIFECRRKTEFLGTLIKAYKTGTLRINYNNSIGVAIK 883	SLFVLHVQREDNKQKGDVVLQSDHVIETLTKTALSADRVNNININ-QGSITFA 1007	RRSRCQR-RVLLLSDTAIYFIATEKNKDKEDRKKRPWIYVQKRRLLLAGITSVELSKLSD 834	EDAKV	KERRRLSIERPYQGDYINYRENFELKD-IVKKNGNEKIMFTHAVNKYD 775	/PRLFISTRLGTE	FTLMSYYYSIQKGAADSMKSN 728	HVRASFLLNLRRQLPRNVLDTSWPTPPPALREASELLRELCMKNMVWKYCRSISPEWKQQ 851	RNKLQRFFLR 707	RQKFLRVKRSAICIQSWWRGTLGRRKAAKRKWAAQTIRRLIRGFILRHSPRCPENAFFLD 791	ESGVETILKSMDLEPKQYSKGKTKIFIRAPETVFNLEELRERKVFTY 697	672 QDGVAVLVRHLGYKPEEYKMGRTKIFIRFPKTLFATEDSLEVRRQSLATKIQAAWRGFHW 731

Search completed: December 9, 2002, 16:45:00 Job time: 32 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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## ALIGNMENTS

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PRINTS; PR00193; myosin_head; 1.

PRODOM; PD000355; myosin_head; 1.

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MYR-2 a novel class-I Myosin identified in rat brain.";

Submitted (AuG-1993) to the EMBL/GenBank/DDBJ databases.

EMBL; X74800; CAA52807.1; -.

HSSP; P08799; IMND.

InterPro; IPR0001609; myosin_head.
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                                                                                        Query Ma
Best Loc
Matches
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"Cloning of myosin I from bovine ad FEBS Lett. 339:31-36(1994).

EMBL; U03420; AAA17565.1; -.

HSSP; P08799; IMND.

InterPro; IPR0010048; IQ_region.

InterPro; IPR001609; myosin_head.
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Q27966;

Q17966;

Q1-NOV-1996 (TrEMBLrel. 01, Created)

Q1-NOV-1996 (TrEMBLrel. 01, Last sequence update)

Q1-NOV-1996 (TrEMBLrel. 21, Last annotation update)

Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)

Myosin I.

Bos taurus (Bovine).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
                                                                                                                                                                                Pfam; PF00612; IQ; 2.
Pfam; PF00063; myosin_head; 1.
PRINTS; PR00193; MYOSINHEAVY.
PRODOM; PD000355; myosin_head; 1.
SMART; SM00015; IQ; 2.
SMART; SM00242; MYSC; 1.
SEQUENCE 1028 AA; 118020 MW; 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=ADRENAL GLAMEDLINE=94148088;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9913;
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                      MESALTARDRVGVQDFVLLENFTSEAAFIENLRRRFRENLIYTYIGPVLVSVNPYRDLQI 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FLLNLRRQLPRNVLDTSWPTPPPALREASELLRELCMKNMVWKYCRSISPEWKQQLQQKA
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                                                                                                                 Similarity
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Pred. No. 0;
25; Mismatches
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                                       SDHVIETLTKTALSADRVNNININQGSITFAGGPGRDGIIDFTSGSELLITKAKNGHLAV 1036
                                                             FLLNLRRQLPRNVLDTSWPTPPPALREASELLRELCMKNMVWKYCRSISPEWKQQLQQKA
                                                                                                                                                          RVKRSAICIQSWWRGTLGRRKAAKRKWAAQTIRRLIRGFILRHSPRCPENAFFLDHVRAS
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RESULT 4 Q28138 ID Q281 AC Q281

Q28138 Q28138;

PRELIMINARY;

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Matches
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01-NOV-1996
01-JUN-2002
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ProDom; PD000355; myosin_head;
SMART; SM00015; IQ; 2.
SMART; SM00042; MYSC; 1.
SEQUENCE 1028 AA; 118241 MW;
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EMBL;
HSSP;
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Pfam; PF00063; myosin_head; 1.
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Bovidae; Bovinae; B
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Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000048; IQ_region.
InterPro; IPR001609; myosin_head.
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                                       SSMNPIMAQCFDKSELSDKKRPETVATQFKMSLLQLVEILRSKEPAYIRCIKPNDAKQPG
                                                                                                                                                   SEQEEYEAEGIAWEPVQYFNNKIICDLVEEKFKGIISILDEECLRPGEATDLTFLEKLED
                                                                                                                                                                                                                                                               KYLTRLLGVEGTTLREALTHRKIIAKGEELLSPLNLEQAAYARDALAKAVYSRTFTWLVR
                                                                                                                                                                                                                                                                                                      SSINDKSDWKVMRKALSVIDFTEDEVEDLLSIVASVLHLGNIHFAADEDSNAQVTTENQL
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                           SSEIPILGQFFDRSELSDKKRPETVATQFKMSLLELVEILKSKEPAYVRCIKPNDSKQPG
                                                                               TIKQHPHFLTHKLADQRTRKSLDRGEFRLLHYAGEVTYNVTGFLDKNNDLLFRNLKETMC
                                                                                               TVKPHPHFLTHKLADQKTRKSLDRGEFRLLHYAGEVTYSVTGFLDKNNDLLFRNLKETMC
                                                                                                                                                                                                           KINRSLASKDAESPSWRSTTVLGLLDIYGFEVFQHNSFEQFCINYCNEKLQQLFIELTLK
                                                                                                                                                                                                                                                 KYLTRLLGVEGSTLREALTNRKTIAKGEELLSPLNLEQAAYARDALAKAVYSRTFTWLVA
                                                                                                                                       SEQEEYEAEGIAWEPVQYFNNKTICDLVEEKFKGIISILDEECLRPGEATDLTFLEKLED
                                                                                                                                                                                             KIKRSLASKDAESPSWRSTTVLGLLDIYGFEVFQHNSFEQFCINYCNEKLQQLFIELTLK
                                                                                                                                                                                                                                                                                                                                                               HILSYLLEKSRVVHQNHGERNFHIFYQLLEGGEEETLRRLGLERNPQSYLYLVKGQCAKV
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P08799; LMND.
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Structure of a mammalian myosin I-beta.";
Batl. Acad. Sci. U.S.A. 91:6349-6353(1994).
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7; Mismatches
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annotation
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Query Match
Best Local
                          InterPro; IPR001609; myosin_head Pfam; PF00612; IQ; 2. Pfam; PF00063; myosin_head; 1. PRINTS; PR00193; MYOSINHEAVY. ProDom; PD000355; myosin_head; 1 SMART; SM002015; IQ; 2. SMART; SM002015; IQ; 2. SMART; SM002042; MYSC; 1. SEQUENCE 1028 AA; 118830 MW;
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Q92002;
01-NOV-1996 (Tr
01-NOV-1996 (Tr
01-JUN-2002 (Tr
Myosin I beta.
                                                                                              InterPro;
InterPro;
                                                                                                                Solc C.F., Derfler B.H., Duyk Aud. Neurosci. 1:63-75(1994). EMBL; U14549; AAA57192.1; -. EMBL; U14382; AAA65091.1; -. HSSP; P08799; 1MND.
                                                                                                                                                                                          MEDLINE-95083594; PubMed-7991542; Metcalf A.B., Chelliah Y., Hudspeth A.J.; "Molecular cloning of a myosin I beta isozyme that madaptation by hair cells of the bullfrog's internal Proc. Natl. Acad. Sci. U.S.A. 91:11821-11825(1994).
                                                                                                                                                                                                                                                                                Rana catesbeiana (Bull frog).
Eukaryota; Metazoa; Chordata;
Amphibia; Batrachia; Anura; Ne
                                                                                                                                                                                                                                                                                                                                                                                                                     1021
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Similarity
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                                                                                              myosin_head
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Anura; Neobatrachia;
 81
79
                             118830 MW;
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No. 1.
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DB 13;
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        Length 1028;
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Matches

814;

Conservative

112;

Mismatches

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Indels

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61 77

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KYLTRLLGVEGTTLREALTHRKIIAKGEELLSPLNLEQAAYARDALAKAVYSRTFTWLVR
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||:|||||||||||||:|::|:
| YSKQHMERYRGVSFYEVSPHIYAIADNSYRSLRTERKDQCILISGESGAGKTEASKKILQ
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                                                  SDHVIETLTKVAITAEKINNININQGSIKFTVGPGKEGIIDFTAGSELLIAKAKNGHLSV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda;
Pterygota; Neoptera; Endopterygota; Diptera; Brachyce
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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MY061F.
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                                                                                     LTFLEKLEDTVKPHPHFLTHKLADQKTRKSLDRGEFRLLHYAGEVTYSVTGFLDKNNDLL
                                                                                                                                                                                       SRTFTWLVRKINRSLASKDAESPSWRSTTVLGLLDIYGFEVFQHNSFEQFCINYCNEKLQ
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 KPNDAKQPGREDEVLIRHQVKYLGLMENLRVRRAGEAYRRKYEAFLQRYKSLCPETWPMW
                                                                                                                          QLFIELTLKSEQDEYRREGIEWIPVEYFDNKVICNLIEEKHKGIISILDEECLRPGEPTD
                                                                                                                                                                          DRLFSWLVQRLNISLQAKETRA---SRNNVMGILDIYGFEIFQKNSFEQFCINFCNEKLQ
                                                                                                                                                                                                                          AKVNSRDLVVTAARLLGVNASELEAALTHRTIDARGDVVTSPLNQELAIYARDALAKAVY
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(TrEMBLrel.)
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Pred. No. 1.8e-
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InterPro: IPR001609; myosin_head.
Pfam; PF00612; IQ. 2.
Pfam; PF00063; myosin_head; 1.
PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head; 1.
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Q63357;
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"Rat myr4 defines a novel subclass of myosin I: Identification, distribution, localization, and mapping of calmodulin-binding sites with differential calcium sensitivity.";
J. Cell Biol. 126:375-389(1994).
EMBL; X71997; CASO871.1; -.
HSSP; P08799; IMND.
                                                                                                                                                                                        SMART; SM00015; IQ; 1
SMART; SM00242; MYSC;
SEQUENCE 1006 AA;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HGHFSSRKTCASDKILEFDR-DFRIRHYAGDVVYSVIGFIDKNKDTLFQDFKRLMYNSSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SRVIVQQPGERSFHSFYQLLQGGSEQMLHSLHLQKSLSSYNYIRVGAQLK-SSINDAAEF
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Matches 405
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01-NOV-1996
01-NOV-1996
01-JUN-2002
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Eukaryota; Metazoa; Nematoda; Chromadorea;
Eukaryota; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cope M.J.T.V., Kendrick-Jones J.;
Submitted (NOV-1993) to the EMBL/
EMBL; 235603; CAA84673.1; -.
EMBL; X75564; CAA53244.1; -.
HSSP; P08799; 1MND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00612; IQ; 1.
Pfam; PF00063; myosin_head; 1.
PFINTS; PR00193; MYOSINHEAVY.
ProDom; PD000355; myosin_head;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Lloyd C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rhabditidae; Peloderinae; NCBI_TaxID=6239;
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MCEIA.
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SMART; SM00242; MYSC; 1.
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                                                                                                                                                                                                                             AEVQTALRSIHTFDKQDVESMWSVIAGLIHLGNVRFIDGENSSGAVHIAEKAALQNAARC
                                                                                                                                                                                                                                           SRVVHQNHGERNFHVFYQLLEGGEEETLRRLGLERNPQSYLYLVKGQCAKVSSINDKSDW
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                                                                                                                                                                                                                                                                                                                                                                                                                                   GVEDLVLLSTIDLKSV-VQNLQLRFQKGRIYTYIGEVLVAVNPYRQLGIYEKSTVDQYKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                           GVQDFVLLENFTSEAAFIENLRRRFRENLIYTYIGPVLVSVNPYRDLQIYSRQHMERYRG
                       HYTSRNL--KQSDKSMGFEEFKITHYAGDVTYSVMGFMDKNKDTLFQDLKRLLYHSKNRL
                                                                       EAEGIAWEPVQYFNNKIICDLVEEKFKGIISILDEECLRPGEATDLTFLEKLEDTVKPHP
                                                                                                                         SVQN--SSRYSKSHVIGVLDIYGFEIFGTNSFEQLCINYCNEKLQQLFIELVLKQEQEEY
                                                                                                                                                                                                  LGVEGTTLREALTHRKIIAKGEELLSPLNLEQAAYARDALAKAVYSRTFTWLVRKINRSL
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MAQCE - -
                                     HFLTHKLADQKTRKSLDRGEFRLLHYAGEVTYSVTGFLDKNUDLLFRNLKETMCSSMNPI
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405; Conserv
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       PRINTS; PR00452; SH3DOMAIN.
ProDom; PD000066; SH3; 1.
ProDom; PD000355; myosin_head; 1
SMART; SM00015; IQ; 1.
SMART; SM00242; MYSc; 1.
SMART; SM00226; SH3; 1.
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090748; 01-NOV-1996 (TrEMBLrel. 0
01-NOV-1996 (TrEMBLrel. 0
01-JUN-2002 (TrEMBLrel. 2
                                                                       PRINTS; PRINTS;
                                                                                                                                                                         Knight A.E., Kendrick-Jones J.;
"A novel vertebrate myosin I.";
Submitted (FEB-1993) to the EMBL/GenBank/DDBJ-:-SIMILARITY: CONTAINS 1 SH3 DOMAIN.
EMBL; X70400; CAAA9850.1; -.
HSSP; P08799; IMND.
                                                                                  Pfam; PF00063; myosin_head; 1
Pfam; PF00018; SH3; 1.
PRINTS; PR00193; MYOSINHEAVY.
                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; c
Archosauria; Aves; Neognathae;
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                                                                                                                        Pfam; PF00612; IQ;
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InterPro; IPR001609; myosin_he
                                                                                                                                                                                                                                                   TISSUE=INTESTINE;
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                                                                                                                                                                                                                                                                                        NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                      Brush border
                                                                                                                                      InterPro; IPR001452;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEP---IQYAVPVVKYDRKGYKPRPRQLLLTPSAVVIVEDAK----VKQRIDYANLTGISV
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PS50002;
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SH3;
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Neognathae; Galliformes; Phasianidae;
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                                                                                                                                     myosin_head.
SH3.
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           REDNKQKGDVVLQSDHV-----IETLTKTALSADRVNNININQGSITFAG-GPGRDGII
                                                                        IKRDFILTPKYFYLIGREKVKKGPEKGQIKEVLKKKVEIQAVSGVSLSTRQDDFFILH--
                                                                                                                                                                                        ASEIFKGKKDNYPQSVPRLFISTRLGTEEISPRVLQSLGS-EPIQYAVPVVKYDRKGYKP
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                                                                                                                           RPRQLLLTPSAVVIVEDAKV------
                                                                                                                                                               ASSILYNEKERRRNSINRNEVGDYLGMEE-RPELRQELAKRERIDFADSITKYDRR-FKP
                                                                                                                                                                                                                                                                                           LLNLRRQLPRNVLDTSWPTPPPALREASELLRELCMKNMVWKYCRSISPEWKQQLQQKAV
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                                                                                                                                                                                                                                                                                                                                                                                                                            LLRSVNMDPDQYQMGRSKVFVKNPESLFLLEEMRERKFDGFARVIQKAW--
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396; Conserv
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Pred. No. 1.1e-109;
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                                                                                                                  KQRIDYANLTGISVSSLSDSLFVLHVQ
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Best Local S
Matches 398
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SH3 domain.
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01-NOV-1996
01-JUN-2002
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ProDom; PD000355; myosin_head;
SMART; SM00242; MYSC; 1.
SMART; SM00326; SH3; 1.
PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-95018277; PubMed-7932763;
MEDLINE-95018277; PubMed-7932763;
Benment W.M., Wirth J.A., Mooseker M.S.;
"Cloning and mRNA expression of human unconventional homologue of amoeboid myosins-I with a single IQ moti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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Submitted (SEP-1994) to the EMBL/GenBank/DDBJ-1-SIMILARITY: CONTAINS 1 SH3 DOMAIN.
EMBL; U14391; AAA62667.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR00193; MYOSINHEAVY PRINTS; PR00452; SH3DOMAIN.
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InterPro; IPR001609; myosin_head.
InterPro; IPR001452; SH3.
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Mammalia; Eutheria;
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Homo sapiens (Human)
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les 398; Conserv
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TLHAMNVIGIFAEEQTLVLQIVAGILHLGNISF-KEVGNYAAVESEEFLAFPAYLLGINQ
                           MRKALSVIDFTEDEVEDLLSIVASVLHLGNIHFAADEDSNAQVTTENQLKYLTRLLGVEG
                                                                                                                                                                        GVQDFVLLENETSEAAFIENLRRRFRENLIYTYIGPVLVSVNPYRDLQIYSRQHMERYRG
                                                                                                              VVHQNHGERNFHVFYQLLEGGEEETLRRLGLERNPQSYLYLVKGQCAKVSSINDKSDWKV
                                                                                                                                                                                                                                                                VSFYEVPPHLFAVADTVYRALRTERRDQAVMISGESGAGKTEATKRLLQFYAETCPAPER 147
                                                                                                                                                                                                                                                                                                                                                 GVDDMVLLSKIT-ENSIVENLKKRYMDDYIFTYIGSVLISVNPFKQMPYFGEKEIEMYQG
                                                                                     VVMRNPGERSFHIFYQLIEGASAEQKHSLGI-TSMDYYYYLSLSGSYKVDDIDDRREFQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF00612; IQ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1109 AA; 127040 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                     31.8%; Score 1715; DB 4; ilarity 37.4%; Pred. No. 2.2e-109; Conservative 172; Mismatches 295;
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C (TrEMBLrel.
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Last sequence update)
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MYO1F.
MEDLINE-21664126; PubMed-11804589;
MEDLINE-21664126; PubMed-11804589;
Krugmann S., Anderson K.E., Ridley S.H., Risso N., McGregor Coadwell J., Davidson K., Eguinoa A., Ellson C.D., Lipp P., Manifava M., Ktistakis N., Painter G., Thuring J.W., Cooper
                                                                                                         MYOSI:...
MYOSIF:
Homo sapiens (Human).
Homo sapiens (Human).
Horia; Metazoa; Chordata;
Horia; Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LVRHLGYKPEEYKMGRTKIFIRFPKTLFATEDSLEVRRQSLATKIQAAWRGEHWRQKFLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KPHPHFLTHKLADQKTRKSLDRGEFRLLHYAGEVTYSVTGFLDKNNDLLFRNLKETMCSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SKDAESPSWRSTTVLGLLDIYGFEVFQHNSFEQFCINYCNEKLQQLFIELTLKSEQEEYE
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                                                                                                                                                                                                                                                                                                                                                            PGVQGAGSRQVQFHQGFGDLAVLKPSNKVLQVSIGPGLPKNSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LLNLRRQLPRNVLDTSWPTPPPALREASELLRELCMKNMVWKYCRSISPEWKQQLQQKAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELPFIKSLFPENLQADKKGRPTTAGSKIKKQANDLVSTLMKCTPHYIRCIKPNETKKPRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VKRDLLLTPKCLYLIGREKVKQGPDKGLVKEVLKRKIEIERILSVSLSTMQDDIFILHEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RPRQLLLTPSAVVIVEDAKVKQ------RIDYANLTGISVSSLSDSLFVLHVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----LNKKERRRNSINRNFIGDYIGMEE-HPELQQFVGKREKIDFADTVTKYDRR-FKG
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(TrEMBLrel.)
(TrEMBLrel.)
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Last sequence up
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                                                                                                                        Craniata; V
Catarrhini;
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                                                                                                                                        Vertebrata;
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on update)
                                                                                                                        Hominidae;
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     Cooper M.A.
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Best Local Similarity
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PRINTS; PR00193; MYOSINHEAVY.

PRINTS; PR00153; WYOSINHEAVY.

PRODOM; PR00056; SH3; 1.

ProDom; PD000355; myosin_head; 1

SMART; SM00242; MYSC; 1.

SMART; SM00326; SH3; 1.

PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Myosin.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00063; myosin_head; Pfam; PF00018; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000637; AT_hook.
InterPro; IPR000048; IQ_region.
InterPro; IPR001609; myosin_head.
InterPro; IPR001452; SH3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and Rho GTPases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00612; IQ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AJ310570; CAC83948.1;
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              RFDEVLIRHQVKYLGLMENLRVRRAGFAYRKKYEAFLQRYKSLCPETWPMWAGRPQDGVA
                                              VKPHPHFLTHKLADQKTRKSLDRGEFRLLHYAGEVTYSVTGFLDKNNDLLFRNLKETMCS
                                                                                                                                               VQEGIRWTPIQYFNNKVVCDLIENKLSPPGIMSVLDDVCATMHATGGGADQTLLQKLQAA
                                                                                                                                                             EAEGIAWEPVQYFNNKIICDLVEEKFK--GIISILDEECL---RPGEATDLTFLEKLEDT
                                                                                                                                                                                                                                                               GTTLREALTHRKIIA----KGEELLSPLNLEQAAYARDALAKAVYSRTETWLVRKINRSL
                                                                                                                                                                                                                                                                                                                MRKALSVIDFTEDEVEDLLSIVASVLHLGNIHFAADEDSN-AQVTTENQLKYLTRLLGVE
                                                                                                                                                                                                                                                                                                                                                                VVHQNHGERNFHVFYQLLEGGEEETLRRLGLERNPQSYLYLVKGQCAKVSSINDKSDWKV
                                                                                                                                                                                                                                                                                                                                                                                                                   GGAVRDRLLQSNPVLEAFGNAKTLRNDNSSRFGKYMDVQFDFKGAPVGGHILSYLLEKSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VSFYEVPPHLFAVADTVYRALRTERRDQAVMISGESGAGKTEATKRLLQFYAETCPAPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GVDDMVLLPQIT-EDAIAANLRKREMDDYIFTYIGSVLISVNPFKQMPYFTDREIDLYQG
DWEENRVKHQVEYLGLKENIRVRRAGFAYRRQFAKFLQRYAILTPETWPRWRGDERQGVQ
                                                                                                                                                                                                                                                  SGRLQEKLTSRKMDSRWGGRSESINVTLNVEQAAYTRDALAKGLYARLFDFLVEAINRAM
                                                                                                                                                                                                                                                                                                   TLSAMQVIGIPPSIQQLVLQLVAGILHLGNISFC--EDGNYARVESVDLLAFPAYLLGID
                                                                                                                                                                                                                                                                                                                                                                                                      VQHVKDIILQSNPLLEAFGNAKTVRNNNSSRFGKYFEIQFSRGGEPDGGKISNFLLEKSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQYENPPHIYALTDNMYRNMLIDCENQCVIISGESGAGKTVAAKYIMGYISKVSGGGEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        400;
                                                                                                                                                                                                                                                                                                                                                    VVMQNENERNFHIYYQLLEGASQEQRQNLGL-MTPDYYYYLNQSDTYQVDGTDDRSDFGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9:95-108(2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of ARAP3, a novel PI3K effector regulating both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            by selective
                                                                                              -----NSWSAG-FVIHHYAGKVSYDVSGFCERNRDVLFSDLIELMQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31.8%;
38.1%;
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Pred. No. 2.36
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Tempst P., Stephens
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                               Query Match
Best Local
              Matches
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PRINTS; PR00452; SH3DOMAIN.
ProDom; PD000066; SH3; 1.
ProDom; PD000255; myosin_head;
                                                                                                                                              SMART; SM00242; MYSC; 1.
SMART; SM00326; SH3; 1.
PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                        Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stoeffler H.E., Ruppert C., Reinhard J., Bahler M.;
"A novel mammalian myosin I from rat with an SH3 domain localizes Con A-inducible, F-actin-rich structures at cell-cell contacts.";
J. Cell Biol. 129:819-330(1995).
-i-SIMILARITY; CONTAINS 1 SH3 DOMAIN.
EMBL; X74815; CAA52815.1; -.
                                                                                                                                                                                                                                                                                                             Pfam; PF00063; myosin_head; 1.
Pfam; PF00018; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                 Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                InterPro: IPR000048: IQ_region.
InterPro: IPR001609: myosin_head
InterPro: IPR001452: SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-95247829; PubMed-7730414;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
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                                                                                                                               domain.
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                               Similarity
                                                                                                       1107
            Conservative
                                                                                                       ΑĄ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AADSFLESVEKTEFVSLLCKRFEEATRRPLPLTFSDTLQFRVKKEGW
    31.7%; Score 1712.5;
37.2%; Pred. No. 3.3e
Live 175; Mismatches
                                                                                                    126826
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                                                                                             B9D8FBB0CE047148 CRC64;
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                    P---GRDGIIDFTSG-SELLITKAKNGHLAV-VAPRL--NSR
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                                                                                            VKRDLLLTPKCLYLIGREKVKQGPDKGLVKEVLKRKIEVERILSVSLSTMQDDIFILHEQ
                                                                                                                                            ASDLLLNKKERRRNSINRNFIGDYIGMEE-HPELQQFVGKREKIDFADIVTKYDRR-FKG
                                                                                                                                                                                                                    LLNLRRQLPRNYLDTSWPTPPPALREASELLRELCMKNMVWKYCRSISPEWKQQLQQKAV
                                                                                                                                                                                                                                                                    VKRSAICTQSWWRGTLGRRKAAKRKWAAQTIRRLIRGFILRHSPRCPENAFFLDHVRASF
                                                                                                                                                                                                                                                                                              LLQSVNMDSDQFQLGRSKVFIKAPESLFLLEEMRERKYDGYARVIQKTWRKFVARKKYVQ
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PWSAGGSRQVQFYQGFGDLAILKPSNKVLQVSIGPGLPKNAR
                                                                                                                                                          ASEIFKGKKDNYPQSVPRLFISTRLGTEEISPRVLQSLGS-EPIQYAVPVVKYDRKGYKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VVHQNHGERNFHVFYQLLEGGEEETLRRLGLERNPQSYLYLVKGQCAKVSSINDKSDWKV 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAQYENPPHIYALADSMYRNMIIDRENQCVIISGESGAGKTVAAKYIMSYVSRVSGGGPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GVDDMVLLSKIT-ESSIVENLKKRYMDDYIFTYIGSVLISVNPFKQMPYFGEKEIEMYQG
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                                            EYDSLLESVFKTEFLSLLTKRYEEKTQKQLPLKFSNTLELKLKKENWG
                                                                                                                     -RIDYANLTGISVSSLSDSLFVLHVQ
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Q9NGL7;
01-OCT-2000
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Amoeboid myosin I (Fragment).
Strongylocentrotus purpuratus (Purple sea urchin).
Eukaryota, Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea, Euechinoidea; Echinocea; Echinoidea; Strongylocentrotidae;
Strongylocentrotus.
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MEDLINE=20440049; PubMed=10984411;
Sirotkin V., Seipel S., Krendel M.
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NON_TER 1053 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Characterization of sea urchin unconventional myosins and their patterns of expression during early embryogenesis."; Mol. Reprod. Dev. 57:11-126(2000).

MBL: AF248488; AAF71717.1;
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                                                                                                                                                                                                                   KSEQEEYEAEGIAWEPVQYFNNKIICDLYEEKF-KGIISILDEECL---RPGEATDLTFL 491
                                                                                                                                                                                                                                                                                                                                  RKINRSLASKDAESPSWRSTTVLGLLDIYGFEVFQHNSFEQFCINYCNEKLQQLFIELTL 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRLLGVEGTTLREALTHRKIIA----KGEELLSPLNLEQAAYARDALAKAVYSRTFTWLV 375
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                         KETMCSSMNPIMAQCF-DKSELSDKKRPETVATQFKMSLLQLVEILRSKEPAYIRCIKPN
                                                                                  QKMNSAVGTHQHY-----
                                                                                                                  EKLEDTYKPHPHFLTHKLADQKTRKSLDRGEFRLLHYAGEVTYSVTGFLDKNNDLLFRNL 551
                                                                                                                                                                                                                                                                                                   SSINGAMQKQKVE-----ITIGVLDIYGFEIFQQNGFEQFCINFVNEKLQQIFIELTL
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-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
EMBL; AF051353; AAC98089.1; -.
HSSP; P08799; IMND.
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ProDom; PD0000355; myosin_head
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e heavy chain of Acanthamoeba myosin IB is a
non-myosin-like sequences.";
c. Natl. Acad. Sci. U.S.A. 84:6720-6724(1987)
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                       YKPRPRQLLLTPSAVVIVE------DAKV-----KQRIDYANLTGISVSSLSDSLF
                                                                        AVASEIFKGKKDNYPQSVPRLFISTRLGTEEISPRVLQSLGSEPIQYAVPVVKYDRK--G
                                                 -----FKTDYINYRQNFK---LKDCIGDK------GTEKVLFADLCNNLDKSFWG
                                                                                                          --- LSLERP
                                                                                                                           SFLLNLRRQLPRNVLDTSWPTPPPALREASELLRELCMKNMVWKYCRSISPEWKQQLQQK
                                                                                                                                                      YEVKKGG-----NDALVNKKERRR------
                                                                                                                                                                           LRVKRSAICIQSWWRGTLGRRKAAKRKWAAQTIRRLIRGFILRHSPRCPENAFFLDHVRA 795
                                                                                                                                                                                                    AILNHVGMSLGKEYQKGKTKIFIRQPESVFSLEELRDRTVFSYANKIQRFLRKTAMRKYY
                                                                                                                                                                                                                    RFDEVLIRHQVKYLGLMENLRVRRAGFAYRRKYEAFLQRYKSLCPETWPMWAGRPQDGVA 676
                                                                                                                                                                                                                                                                                                       SSTFFAGLFPEAKEVATSKKKPTTAGFKIKESINILVATLSKCTPHYIRCIKPNEKKAAN
                                                                                                                                                                                                                                                                                                                         MNPIMAQCFD--KSELSDKKRPETVATQFKMSLLQLVEILRSKEPAYIRCIKPNDAKQPG
                                                                                                                                                                                                                                                                                                                                                      PTHAHLAATSQPD-----EFVIKHYAGDVVYNVDGFCDKNKDLLFKDLIGLAECT
                                                                                                                                                                                                                                                                                                                                                                   KPHPHFLTHKLADQKTRKSLDRGEFRLLHYAGEVTYSVTGFLDKNNDLLFRNLKETMCSS
                                                                                                                                                                                                                                                                                                                                                                                                                   EEYEAEGIAWEPVQYFNNKIICDLVEEKF-KGIISILDEECLRPGEATDLTFLEKLEDTV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RSLASKDAESPSWRSTTVLGLLDIYGFEVFQHNSFEQFCINYCNEKLQQLFIELTLKSEQ
                                                                                                                                                                                                                                                                                                                                                                                                      EEYGAEGIQWENIDYFNNKICCDLIEEKRPPGLMTILDDVCNFP-KGTDDKFREKLLGAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DAMY IDDPEA-----LTTGILDFYGFEIFGKNGFEQLCINFVNEKLQQIFIQLTLKAEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PVAVEQALLYR-TITTGEQGRGRSSVYSCPQDPLGAIYSRDALSKALYSRMEDYIIQRVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DVMRVKDVILESNPLLEAFGNAKTIRNNNSSRFGKYMEIQFDLKGDPVGGRISNYLLEKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DTWNAMKVIGETABEQHEIFRLVTAILYLGNVQFVDDGKGGSTIADRQVVEMLAYLMRTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VMRKALSVIDFTEDEVEDILSIVASVLHLGNIHFAADEDSNAQVTTENQLKYLTRLLGVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RVVYQTNGERNFHIFYQLLAGAPADLRQEFGLQ-TPDYYFYLNQGKTYTVDGMDDNQEFQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RGGAVRDRLLQSNPVLEAFGNAKTLRNDNSSRFGKYMDVQFDFKGAPVGGHILSYLLEKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GKYRYELPPHVYALADDMYRTMLSESEDQCVIISGESGAGKTEASKKIMQYIAAVSGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GVSFYEVPPHLEAVADTVYRALRTERRDOAVMISGESGAGKTEATKRLLQFYAETCPAPE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GVDDMVMLTSISND-AINDNLKKRFAADLIYTYIGHVLISVNPYKQINNLYTERTLKDYR
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373; Conserv
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%; Pred. No. 1.4e-99;
165; Mismatches 304; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E37AD44A685803A6 CRC64;
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RESULT 15
Q19901
Q19901
Q19901
AC Q19901
D1 NOV-1996 (TrEMBLrel 01)
DT Q1-NOV-1996 (TrEMBLrel 01)
DT Q1-NOV-1996 (TrEMBLrel 21)
DE F29D10.4 protein.
GN GENCALYOLA; Netazoa; Nematc
CC Rhabditidae; peloderinae;
RN [1]
RP SEQUENCE FROM N.A.
RA White S.;
RI SUBMITTED FROM N.A.
RA White S.;
RI SEQUENCE FROM N.A.
RA White S.;
RT GENOME SEQUENCE of the n.
Investigating biology.";
RI SECIENCE 282:2012-2018 (199)
CC -1- SIMILARITY: CONTAINS
RA NONE;
RT GENOME SEQUENCE Of the n.
RT GENOME SEQUENCE OF THE NONE OF 
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                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00063; myosin_head; 1.
Pfam; PF00018; SH3; 1.
PRINTS; PR00193; MYOSINHEAVY.
ProDom; PD000066; SH3; 1.
ProDom; PD000355; myosin_head;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 282:2012-2018(1998).
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
EMBL; 275952; CAB00095.1; -.
HSSP; P08799; 1MND.
               193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50002; SH3; 1.
PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
                                                                                                          133
                                                             207
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Rhabditidae; Peloderinae;
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                                                                                                                                                                                                           73
                                                                                                                                                                                                                                                         87
                                                                                                                                                                                                                                                                                                                        27 VGVQDFVLLENFTSEAAFIENLRRRFRENLIYTYIGPVLVSVNPYRDLQIYSRQHWERYR 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       875
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      959 VLHVQREDNKQKGDVVLQSDHVIETLTKTAL---
RVVHQNEGDRNFHVFYQLCAGADKNLRSTFGI-GELQYYNYLNMSGVFKADDTDDGKEFE
                                             RVVHQNHGERNFHVFYQLLEGGEEETLRRLGLERNPQSYLYLVKGQCAKVSSINDKSDWK 266
                                                                                                                                                                                                                                            GVSFYEVPPHLFAVADTVYRALRTERRDQAVMISGESGAGKTEATKRLLQFYAETCPAPE 146
                                                                                                KVQHIKDVILQSNPLLEAFGNSATVRNWNSSRFGKYVEIVFSRGGEPIGGKLSNFLLEKS
                                                                                                                                                                                            GAAQYENAPHIYALADNMYRNMLIDNESQCVIISGESGAGKTVNAKFIMNYISRISGGGQ 132
                                                                                                                          VGVDDMVLLPKLT-EQSIVENLKKRLQANSIFTYIGPVLISVNPFKQMPYFTEKEMLLYQ
                                                                                                                                                                                                                                                                                                                                                                                                          367;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TLKGGKTCVVKFIRDPQGGDGKVKGTKVS
                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (JUL-1996) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                       Conservative 172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=9851916,
                                                                                                                                                                                                                                                                                                                                                                                                                              29.0%;
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SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124885 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oda; Chromadorea;
Caenorhabditis.
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                               Score 1564; DB 5;
Pred. No. 5.7e-99;
2; Mismatches 320;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2CDB6F02EDEEDED9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1100;
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  251
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рь	Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy	рь	Оy	рь	Qy	DЪ	Qy	Db	Qy	Db	ОУ	Db	Qy	Ь	Qy	ДЬ	QУ	Вb	Qy
887	1005	837	963	777	916	720	858	711	798	711	738	656	678	596	618	536	559	488	499	428	443	371	383	311	327	252	267
DFSDGKRTVQFGNDGTSSAEKTLKPNGKVLNVS 919	TFAGGPGRDGIIDFTSGSELLITKAKNGHLAVVA 1038	GNDDYSSLLETPFKTEFCTALSKAYKERTNGTLHLDFRSSHVVSYKKMKF 886	QREDNKQKGDVVLQSDHVIETLTKTALSADRVNNININQGSI 1004	VTKLDLLLTVNHLTLIGKEKVKNGPEKGKIVEVIKRQFDLPQIKSIGLSPYQDDFVILYL 836	PRPRQLLLTPSAVVIVEDAKVKQRIDYANLTGISVSSLSDSLFVLHV 962	AADLMYGKKERRRYSLNRNFVGDYIGLEHHPTLQSLVGKRQRVLFACTANKYDRK-FR 776	ASEIFKGKKDNYPQSVPRLFISTRLGTEEISPRVLQSLGSEPIQYAVPVVKYDRKGYK 915	719	LLNLRRQLPRNVLDTSWPTPPPALREASELLRELCMKNMVWKYCRSISPEWKQQLQQKAV 857	710	VKRSAICIQSWWRGTLGRRKAAKRKWAAQTIRRLIRGFILRHSPRCPENAFFLDHVRASF 797	ICDSVHMEKNQYQMGKTKIFVKNPESLFLLEETRERKFDGYARVIQKAWRQESAR 710	T	WEESRVKHQVEYLGLRENIRVRRAGFAYRRAFDKFAQRYAIVSPQTWPCFQGDQQRACEI 655	FDEVLIRHQVKYLGLMENLRVRRAGFAYRKYEAFLQRYKSLCPETWPMWAGRPQDGVAV 677	SRPFIQALFPENVAASAGKRPTTFSTKIRTQANTLVESLMKCSPHYVRCIKPNETKRPND 595	MNPIMAQCFDKS-ELSDKKRPETVATQFKMSLLQLVEILRSKEPAYIRCIKPNDAKQPGR 617	AGHPHFGPGSDSFVIKHYAGDVTYNVDGFCDRNRDVLYPDLILLMQKS 535	TGFL	VREGIKWTEIDYFDNKIVCDLIETKRPPGIMSLLDDTCAQNHGQREGVDRQLLTTLSKSF 487	EAEGIAWEPVQYFNNKIICDLVEEKF-KGIISILDEECLRPGEATDLTFLEKLEDTV 498	NITSQSTSDNFSVGILDIYGFEIFNNNGFEQFCINFVNEKLQQIFIELTLKAEQEEY 427	NHO	SADIEAKLTGRKMESKWGTQKEEIDMKLNVEQASYTRDAWVKAIYARLFDYLVKKVNDAM 370	GTTLREALTHRKIIAKGEELLSPLNLEQAAYARDALAKAVYSRTFTWLVRKINRSL 382	STLHAMKVVGVNDQDQLEVLRIVATVLHIGNITF-TEENNFAAVSGKDYLEYPAFLLGLT 310	VMRKALSVIDFTEDEVEDLLSIVASVLHLGNIHFAADEDSNAQVTTENQLKYLTRLLGVE 326

Search completed: December 9, 2002, 16:46:44 Job time : 89 secs

